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version 5.1.6
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 GenCore (c) 1993 -
           Copyright
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1 NIJVQFGVMIEKMIGKSALQY.......YNRKYAHYPNKLCTGPTPPC 123 US-10-088-092A-30\_COFY\_20\_142 Title: Perfect score:

Sequence:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\* A Geneseq 29Jan04: geneseqp2004s; Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aab81022 Human pho Abr44235 Human sec Abb63125 Human gro Aab12810 Mouse sec Aab81021 Murine ph Ada61984 Human IBM Aar10126 Membrane-Description Aaw73562 Ada61982 Ada61978 Abr83569 Aap93112 Aap93363 Aar25416 ABR44235 ABU63125 AAB12810 AAB81021 ADA61984 AAR10126 AAW73562 ADA61982 ADA61978 ABR83569 AAP93112 AAP93363 AAB81022 ü DB Query Match Length Result Š.

Abb08154 Murine PL			N	LO.			Abr44236 Human sec		Human	Human	Human	. ~		2 Solid	6 Phosph			Human	Human
ABB08154	ABP96808	AAR63053	AAY88292	AAW58476	AAB12536	AAB11994	ABR44236	ABR44231	ABU63121	ADB65581	ABB08202	ABR48182	AAE38590	AAW99582	AAR39346	AAR63046	ABR44237	AAE37571	ABU63126
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146	146	145	122	132	144	144	168	168	168	168	211	211	211	118	122	138	138	138	138
7.2	7.2	9	5.9	3.6	43.1	43.1	42.0	42.0	2.0	2.0	2.0	2.0	42.0	1.5	41.5	41.5	1.5	41.5	1.5
4.	4	4	4	4										4	4	4	4	4	4,
341	341	338.5	331.5	314.5	311	311	303	303	303	303	303	303	303	299.5	299.5	299.5	299.5	299.5	299.5
26	27	28	29	30	37	32	33	34	32	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

Human phospholipase A2 (PLA2) amino acid sequence. Æ AAB81022 standard; protein; 142 (first entry) 12-JUN-2001 AAB81022 

Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antiinfilammatory; tranquilliser; antiasthmatic; antiallergic; trauma; antirheumatic; antiarthritic; septic shock; panoreatitis; human; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.

Homo sapiens

20. .142 /label= Mature\_PLA2 /note= "Mature\_phospholipase A2" 1. .19 /label=\_Signal\_peptide Location/Qualifiers WO200121775-A1 Key Peptide Protein

29-MAR-2001

18-SEP-2000; 2000WO-JP006344. 99JP-00266616 21-SEP-1999;

SHIO ) SHIONOGI & CO LTD

Human gro Human G72 Human BLA Human inf Human syn PLA2. 1/1 Human PLA

Hanasaki K; Ishizaki J, Suzuki N,

WPI; 2001-290432/30. N-PSDB; AAF77401.

ĕ Human secretory phospholipase A2 and encoded gene, useful in diagnosis and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid

Aar63055 Human PLA Abry4433 Human sec Abp96807 Human pho Abu63123 Human gro Adb75501 Prostate Ade63560 Human Pro Aab56432 Human pro Ada61983 Human T10 Aar63608 Rat PLA2 Ade63558 Rat Prote Aaw08368 Mouse PLA

Human pho Human gro Prostate

ABP96807 ABU63123 ADB75501

ADE63560

ADA61983 AAR63060 ADE63558 AAW08368

Claim 1; Page 46-47; 50pp; Japanese.

A2 (PLA2) protein This invention relates to human secretory phospholipase

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Sequence 154 AA;
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ABU63125
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and the gene encoding it. Inhibitors of phospholipase A2 have antibacterial; immunosuppressive; antiinflammatory; tranquilliser; vulnerary; antiathatic, antiantermatic; and antiarthritic activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in the diagnosis of PLA2 associated diseases e.g. septic shock, adult respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinitis and rheumatoid arthritis. The present sequence represents human PLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group IIF secreted phospholipase A2; sPLA2; phosphatidy1glycerol; human;
phosphatidy1choline; antibacterial; virucide; cytostatic; vasotropic;
antiinflammatory; vulnerary; cardiant; chromosome 1p35; transgenic;
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                                                                                                                                                                                                                                                                                                                                      Length 142;
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                                                                                                                                                                                                                                                                                                                                   100.0%; Score 722; DB 4;
100.0%; Pred. No. 8.5e-59;
ive 0; Mismatches 0;
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Matches 123; Conservative
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                                                                                                                                                                                                                                                                                    Sequence 142 AA;
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apoptosis is useful for treating disease states or disorders involving group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain scanemia, acute lung injury, acute respiratory distress syndrome or Crohn's disease. Specific antibodies are useful for searching new secreted mammalian group IIF sPLA2 or the homologues of the enzyme in other mammals. The encoding polynucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals. Sequences ABR44322-238 represent various human secreted sPLA2 enzymes used in alignment studies with the GIIF sPLA2 enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                      92 KLEKYLFSVSERGIFCAGRITCQRLICCDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT
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100.0%; Pred. No. 9.1e-59;
ive 0; Mismatches 0;
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(LAMB/) LAMBEAU G.
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             a 15-fold preference. The mammalian secreted group IIF spiaz protein or nucleic acid, or a pharmaceutical composition is useful for treating and/or preventing viral infections, or cancers. The inhibitors of SPIAZ or a composition comprising spiaz inhibitors is unbibitors of sPIAZ or a composition comprising spiaz inhibitors is useful for treating disease states or disorders involving group IIF sPIAZ, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome, or Crohn's acute lung injury, acute respiratory distress syndrome, or Crohn's compounds for treating these diseases. This is the amino acid sequence of human group IIE phospholipase A2 used to determine a consensus sequence
                                                                                                                                                                                                                                                                                                                                                                          KLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 120
 phosphatidylcholine with about
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                                                                                                                                                                                                                                                                                                                               32 NLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding mouse secretory type phospholipase A2 (PLA2) g for inhibitors of PLA2.
                                                                                                                                                                                                                                               Length 154;
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                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                           100.0%; Score 722; DB 6; 100.0%; Pred. No. 9.1e-59;
phosphatidylglycerol versus
                                                                                                                                                                                                                                                                            Mismatches
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N-PSDB; AAA73130.
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                             for human sPLA2s
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                                                                                                                                                                                                              Sequence 154 AA;
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AAB12810
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DB 3; Length 142;

91.7%; Score 662;

Query Match

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                                                                                                                                    80 KLEKYLPSITRDNIFCAGRIACQRHTCECDKRAALCFRHNLMTYNRKYAHYPNKLCTGPT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secretory phospholipase A2 and encoded gene, useful in diagnosis of and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid
                                                   9
                                                                                 79
                                                                                 20 NIVOFGVMIERMIGKPALOYNDYGCYCGVGGSHWPVDETDWCCHAHDCCYGRLEKLGCDP
                                                                                                                   61 KLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGPI
                                                                                                                                                                                                                                                                                                                                                                                                                               Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antiinflammatory; tranquilliser; antiasthmatic; antiallergic; tranma; antirheumatic; antiarthritic; specie shock; pancreatitis; mouse; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.
                                                   1 NLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
                   Gaps
                   .;
0
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Murine phospholipase A2 (PLA2) amino acid sequence.
 88.6%; Pred. No. 2.8e-53; ive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20. .142
/label= Mature_PLA2
/note= "Mature_phospholipase A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .19
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                    AAB81021 standard; protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-2000; 2000WO-JP006344.
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD.
nl Similarity 88.6
109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-290432/30.
N-PSDB; AAF77387.
                                                                                                                                                                                  121 PPC 123
                                                                                                                                                                                                               140 PPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200121775-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shizaki J,
                                                                                                                                                                                                                                                                                                                                                                     12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis
                                                                                                                                                                                                                                                                                                                                   AAB81021;
Best Local
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                    AAB8102
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Group IIA PLA2 and an antibiotic. The methods of the invention are useful for killing Gram-positive bacteria, (especially Staphylococcus aureus) and for treating human patient surfering from an infection caused by Gram-positive bacteria. The bacteria are selected from Micrococcus, Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus, Enterococcus, Methanobacterium, Peptostridium, Lactobacillus, Listeria, Erysipelothrix, Corymbacterium, Propionibacterium, Bacterionema, Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolyspora. The methods are useful for treating potentially life-threatening infection caused by multi-drug resistant Gram positive bacteria, for treating wound and bloodstream infection with methicillin-resistant S. aureus (MRRA) and
                                                                                                                                                                                                                                                 nosocomial infections with vancomycin-resistant Enterococcus faecium. The present sequence represents the I8M/G72K/T103K mutant PLA2 of the Invention. Note: The present sequence is not shown in the specification but was created by the indexer using the information in example 1 and the sequence appearing as ADA61978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TKFLSYKFSNSKSRITCAKODSCRSQLCECDKAAATCFARNKKTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human spleen was homogenated then centrifuged to obtain a precipitated pellet comprising the cell membrane component. The pellet was extracted with KBr aq. solution. Pure phospholipase A2 was obtained from the crude preparation by a combination of chromatography techniques. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKLEKYL PSVSERGI FCAGRITCORLITCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human spleen deriving membrane bound phospholipase A2 - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-bound phospholipase A2 from human spleen.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 363.5; DB 6;
Pred. No. 7.5e-26;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human phospholipase A2; anti-inflammatory drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10126 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening antiinflammatory drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 1; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                              50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPPC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TPRC 124
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2; group IIA PLA2; bacterial infection; Staphylococcus aureus; multi-druy resistance; wound; bloodstream infection; methicillin-resistant S. aureus; MRSA; nosocomial infection; vancomycin-resistant Enterococcus faecium; mutein; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to Killing gram-positive bacteria (I) in human patient, comprising contacting the bacteria with a bactericidal-effective amount of mutant human group IIA phospholipase A2 (Group IIA PLA2) appearing as ADA61978, or treating a human patient suffering from infection caused by a bacteria comprising administering a mutant human
                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                     80 KLEKYLPSITRDNIFCAGRTACQRHTCECDKRAALCPRHNLNTYNRKYAHYPNKLCTGPT 139
                                                                                                                                                                                                                79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating a patient suffering from infection caused by gram-positive bacteria or killing gram-positive bacteria, comprises delivering mutant human Group IIA phospholipase A2.
                                                                                                                                                                                                                    20 NLVQFGVMIERMIGKPALQYNDYGCYCGVGGSHWPVDETDWCCHAHDCCYGRLEKLGCDP
                                                                                                                                                                                                                                                             KLEKYLFSVSERGI FCAGRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT
                                                                                                                                                                              1 NLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
                                                                                                                                    Gaps
                                                                                                                                    .
0
                                                                                              Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Gly substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type Thr substituted by Lys"
                                                                                                                                    Indels
                                                                                           Score 662; DB 4;
Pred. No. 2.8e-53;
                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA61984 standard; protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human I8M/G72K/T103K PLA2 mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liang N;
                                                                                           91.7%;
88.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0172467P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                Similarity 88.6
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiss J, Elsbach P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-219013/21.
                                                                                                                                                                                                                                                                                                                                                                                          140 PPC 142
                                                                                                                                                                                                                                                                                                                                                  PPC 123
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Misc-difference
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                                                     Sequence 142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Homo sapiens.
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                                                                                                                  Best Local Sim
Matches 109;
                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                  121
                                                                                              Query Match
               gene
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9

Gaps

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Length 124; Indels and FXa inhibition, which maximizes the effects of drugs based on the

peptide

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60 PKLEKYLFSVSERGIFCAGRITCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                     TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (hsPLA2
                                                                                                                              20
                                                                                                                                                   9
                                                                                                                                         1 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG
                                                                                                                                                                                                                                                                                                                                                                                          Human group II secretory phospholipase A2; hsPLA2 grII; FXa inhibitor; coagulation disorder; haemostatic disorder; FVa/FVa complex formation;
                                                                                                                          1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                       Gaps
can be used as an antigen to generate monoclonal antibodies with specificity against human spleen-derived phospholipase A2. The monoclonal antibodies can be used in the diagnosis of inflammation. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide fragment of human group II secretory phospholipase A2 grII) - useful in the treatment or prevention of coagulation and hemostatic disorders.
                                                                                                       7
                                                                                 DB 2; Length 124;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                    Human group II secretory phospholipase A2 protein.
                                                                               Score 360.5; DB 2;
Pred. No. 1.4e-25;
9; Mismatches 45;
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                                                                                                                                                                                                                                                                                                  AAW73562 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 27; 62pp; English.
                                                                             11arity 55.6%,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-IB000869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0048668P
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mounier C, Hackeng T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-045729/04.
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                    TPPC 123
                                                                                                                                                                                                                                          TPRC 124
                                                       Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1997;
                                                                                                                                                                                                                                                                                                                                               10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9855504-A1
                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1998
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This sequence represents the full length human group II secretory phospholipase A2 (hsPLA2 grII) protein. The invention relates to peptides comprising eleven amino acids, corresponding to residues 51-62 of hsPLA2 grII. The peptides are useful in screening new compounds for their potential use as drugs in the treatment or prevention of coagulation potential use as drugs in the treatment or prevention of coagulation activation in vivo in humans and animals). The peptides and antibodies form compositions in the regulation of the coagulant effect in vivo in humans or animals. The peptides are also useful, in forming kits in the humans or animals. The peptides are also useful, the peptides and antibodies form compositions in the treatment or prevention of haemostatic disorders. The peptide represents the specific region of haemostatic disorders. The peptide represents the specific region of hsPLA2 grII involved in the inhibition of the FVA/FVA complex formation,

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۲,
                                                                                                                                                                                                 60 PKLEKYLFSVSERGIFCAGRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2; group IIA PLA2; bacterial infection; Staphylococcus aureus; multi-drug resistance; wound; bloodstream infection; methicillin-resistant S. aureus; MRSA; nosocomial infection; vancomycin-resistant Enterococcus faecium; mutein; mutent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to killing gram-positive bacteria (I) in human patient, comprising contacting the bacteria with a bactericidal-effective amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2) appearing as ADA61978, or treating a human patient suffering from infection caused by a bacteria comprising administering a mutant human group IIA PLA2 and an antibiotic. The methods of the invention are useful for killing Gram-positive bacteria, (especially Staphylococcus aureus) and for treating human patient suffering from an infection caused by Gram
                                                                                                                                                                                                                     61 TKFLSYKFSNSGSRITCAKQDSCRSQKCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                      1 NIVOFGVMIEKMIGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a patient suffering from infection caused by gram-positive bacteria or killing gram-positive bacteria, comprises delivering mutant human Group IIA phospholipase A2.
                                                                                                                                                        1 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG
                                                                                                              Gaps
                                                                                                              ;
                                                                              DB 2; Length 124;
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Gly substituted by Lys"
                                                                                                            45;
                                                                           Score 360.5; DB 2
Pred. No. 1.4e-25;
9; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       ADA61982 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page; 22pp; English.
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                                                                         Query Match
Best Local Similarity 55.6%;
Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L8-DEC-2000; 2000US-00740569
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human G72K PLA2 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weiss J, Elsbach P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-219013/21
                                                                                                                                                                                                                                                                120 TPPC 123
                                               Æ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                               Sequence 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                        ADA61982;
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positive bacteria. The bacteria are selected from Micrococcus, Staphylococcus, Streptococcus, Peptoaccus, Peptostreptococcus, Enterococcus, Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus, Listeria, Erysipelothrix, Corynebacterium, Propionibacterium, Eutococcus, Methanopees, Arachnia, Bifidobacterium, Bacterionema, Bothia, Mycobacterium, Nocardia, Streptomyces and Micropolyspora. The methods are useful for treating potentially life-threatening infection caused by multi-drug resistant Gram positive bacteria, for treating wound and bloodstream infection with methicillin-resistant S. aureus (MRSA) and nosocomial infections with vancomycin-resistant Enterococcus faecium. The present sequence represents the Aracomycin-resistant Enterococcus faecium. The present sequence is not shown in the specification but was created by the indexer using the information in example 1 and the sequence appearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2; group IIA PLA2; bacterial infection; Staphylococcus aureus; multi-fruy resistance; wound; bloodstream infection; methicillin-resistant S. aureus; MRSA; nosocomial infection; vancomycin-resistant Enterococcus faecium; mutein; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLVNFHRLIKLTTGKEAALSYGFYGCHGGVGGRGSFKDATDRCCVTHDCCYKKLEKRGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.9%; Score 360.5; DB 6; Length 124; 54.8%; Pred. No. 1.4e-25; ive 11; Mismatches 44; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
/note= "Wild-type Thr substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Wild-type Gly substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ADA61978 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G72K/T103K PLA2 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000US-00740569.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weiss J, Elsbach P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-219013/21.
N-PSDB; ADA61977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 TPPC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TPRC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as ADA61978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA61978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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IID -ADA6

AAC ADA6

XXX ADA6

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The invention relates to killing gram-positive bacteria (I) in human patient, comprising contacting the bacteria with a bactericidal-effective amount of mutant human group IIA phospholipase A2 (Group IIA PLA2) appearing as ADA61978, or treating a human patient suffering from infection caused by a bacteria comprising administering a mutant human for properting and an antibiotic. The methods of the invention are useful for killing Gram-positive bacteria. Suffering from an infection caused by Gram footier are selected from Micrococcus,
                                                                                                                                                                                                                                                                      Staphylococcus, Streptococcus, Peptococcus, Enterococcus, Enterococcus, Straptococcus, Peptococcus, Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus, Listeria, Erysipelothrix, Corynebacterium, Propionibacterium, Bacterionema, Bubacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema, Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolyspora. The methods are useful for treating potentially life-threatening infection and bloodstream infection with methicillin-resistant S. aureus (MRSA) and nosocomial infections with vancomycin-resistant Enterococcus faecium. The present sequence represents the G72K/T103K mutant PLA2 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKKTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
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Treating a patient suffering from infection caused by gram-positive bacteria or killing gram-positive bacteria, comprises delivering mutant human Group IIA phospholipase A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PKLEKYLFSVSERGIFCAGRITCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; TolA; TolAIII domain; bcr; Escherichia coli; human;
interaction; cléavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.9%; Score 360.5; DB 6; 54.8%; Pred. No. 1.4e-25; tive 11; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PLA2 amino acid sequence SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UYNE-) UNIV NEWCASTLE VENTURES LTD.
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                                                                                    Claim 1; Fig 3; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2002; 2002GB-00000689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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label= exon\_1

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The present invention describes a fusion polypeptide (I) for expression in a host cell comprising a TolAIII domain (functional homologue, fragment or derivative), and a non-TolA polypeptide, where the TolAIII domain (functional homologue, fragment or derivative) is located towards to chart of the fusion polypeptide, where the TolAIII contains of the fusion polypeptide, and the non-TolA polypeptide is located towards the C-terminus of the fusion polypeptide (I); (2) an corression vector (III) encoding the fusion polypeptide (I); (2) an expression vector (III) comprising (II) for expression of (I); (2) an containt of the TolAIII domain (functional homologue, fragment or comprising the TolAIII domain (functional homologue, fragment or derivative) upstream or downstream from a cloning site which allows incompanies in service of I), and/or (III), and/or (III), and/or (III), and/or (III) or containt of the TolAIII domain (functional homologue, fragment or derivative) is useful for producing the fusion polypeptide (I), band molecule (II), expression vector (III) or containt and properties of the non-TolA polypeptide, or studying interaction properties of the non-TolA polypeptide, or studying interaction properties of the non-TolA polypeptide or the fusion polypeptide as a fusion polypeptide in a host cell. ACPS7145 to and ARRB3514 represent sequence used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 PKLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
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                                           New fusion polypeptides, useful for immobilization or purification and isolation of the non-TolA polypeptide, or for studying interaction properties of the non-TolA polypeptide or the fusion polypeptide, e.g. self-interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLVQFGVMIEKMIGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.9%; Score 360.5; DB 6; Length 124; 55.6%; Pred. No. 1.4e-25; live 9; Mismatches 45; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycerophospholipids; non-pancreatic,
                                                                                                                                                                     Example 1; Page 56-57; 68pp; English
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les 69; Conservative
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WPI; 2003-587105/55
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31-JUL-1992
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Matches
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ID AAP93112
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Location/Qualifiers

Homo sapiens

Peptide Region

1. .20 /label= signal

1. .14

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The protein sequence was deduced from a DNA sequence obtd. from a genomic DNA library which was prepd. from a mutant fibroblast cell line which contains 5 copies of the X chromesome (GM5009). The signal sequence is thought to be incomplete at the N-terminal since no promoter-like sequences are found in the DNA within 100 nucleo-tides 5' of this region. The deduced N-terminal sequence of the mature protein confirmed results obtd. by direct sequencing of the purified protein. This sequence for the mature protein confirmed results obtd. by direct sequencing of the purified protein. This sequence of the purified protein. This sequence (29) and there is a cluster of basic amino acids [e.g. Arg (27), Lys highly conserved lipophilic residues [e.g. Leu (22)] Pla (25), and Ile (29) and there is a cluster of basic amino acids [e.g. Arg (27), Lys (30) and high is believed to be an important determinant in the interaction of Full 2. There is a characteristic stretch of residues which comprises part of the calcium binding loop: Tyr(44)-Gly-Cys-X-Cys-Gly-Cys-X-X-X-Pro(56) and Asp(68). The conserved residues which constitute the active site (see features) are also present, and the protein exhibits the placement of half-cysteine residues typical of a Gp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 NLVNFHRMIKLTIGKERALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLVQFGVMIEKMIGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                                                                                                      "calcium binding loop"
                                                                                                                                                                                                                                                                                                                                                                                    /note= "calcium binding'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hession C;
                                                                                                                                                      "Claim 14"
                                                                                          "Claim 12"
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15. .62 _/
|abel= exon_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99. .124
/label= exon_4
111
                                                                                                                                                                                                                                                    63. .98
/label= exon_3
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/note= "c
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                                                               21. .39
/note= "
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Matches 69; Conserv
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Binding-site
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Active-site
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AAP93363;

RESULT 13

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This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA was amplified using the primer sequences given in AAQ26370-1 by PCR from a human lung cDNA library. The cDNA sequence was used in the construction of an expression vector which further comprised a promoter and a dominant control region. This vector was used in an expression system comprising a mammalian cell transformed with the vector. This expression system could be used to prepare pharmacologically useful polypeptides eg, human growth hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2, and for gene therapy. The mammalian host comprises erythroid cells and a heterologous promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
81 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKXQYYSNKHCRGS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression vectors for use in mammalian cells - contain dominant control region derived from beta-globin gene.
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                                                                                                                                                                                                                                                                                                                                                            Human growth hormone; granulocyte-colony stimulating factor; G-CSF; phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy; erythroid cells; cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grosveld FG, Antoniou M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 360.5; DB 2;
Pred. No. 1.6e-25;
9; Mismatches 45;
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                                                                                                                                                                                                         AAR25416 standard; protein; 144 AA.
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Best Local Similarity 55.6%;
Matches 69; Conservative 9
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N-PSDB; AAQ26372.
                                                                 120 TPPC 123
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                                                                                                         141 TPRC 144
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                                                                                                                                                                                                                                                                                     06-JAN-1993
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AAR25416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone lambda SPiA2cDNA-4 is one of four clones identified when probe oligo 2905 (AAN91257) was used to screen a cDNA library constructed from polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2 type A sequence which is given here. The mature peptide sequence (see FT) has a calculated molecular weight of 13,919 daltons. The same amino acid sequence is also encoded by the exons of clone lambda SPLA2-6 (AAN91260) in Figure 7. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI correct PI
      TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYOYYSNKHCRGS 140
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                                                                                                                                                                                                                                                                                                                                                  Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone lambda SPLA2cDNA-4 and by the exons of clone lambda SPLA2-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          Human synovial phospholipase A2; clone lambda sPLA2cDNA-4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vadas P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 49.9%; Score 360.5; DB 1; Similarity 55.6%; Pred. No. 1.6e-25; 69; Conservative 9; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seilhamer JJ, Pruzanski W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 21. .144
                                                                                                                                                                                                         AAP93363 standard; protein; 144 AA.
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UNIV OF TORONTO INNOVAT.
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88US-00215726.
88US-00231865.
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N-PSDB; AAN91258, AAN91260.
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(first entry)
                                                                     120 TPPC 123
                                                                                                           141 TPRC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                               lambda sPLA2-6.
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06-JUL-1988;
16-AUG-1988;
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27-JUN-1980
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AAP93363
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AAPP 93363
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Protein

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Gaps

7;

Length 144; Indels 140

141 TPRC 144

В

60 PKLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119

Best Loc Matches

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*Novel type III and IV low mol. wt. phospholipase A2 enzymes - from humans and rats, also nucleic acid sequences useful, e.g. for recombinant prodn. of enzymes, research into Batten's disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human cDNA (AAQ81138) expressing a novel PLA2, HPLA2-10, was derived from human brain RNA by RACE-PCR. HPLA2-10 (AAR63346) was characterized as a novel type of PLA2, type IV, on the basis of its Cys content in comparison with human PLA2 types I (AAR63054) and II (AAR63055) (Updated on 25-MAR-2003 to correct PN field.)
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Best Local Similarity 55.6%; Pred. No. 1.6e-25;
Matches 69; Conservative 9; Mismatches 45; Indels 1.
                                                                               AAR63055 standard; protein; 144 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                            HPLA2-10; phospholipase A2; PLA2.
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                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                            Human PLA2 type II.
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26-JUL-1993;
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15-AUG-1995
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AAR63055
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July 3, 2004, 05:17:51 ; Search time 43.6302 Seconds (without alignments) 877.555 Million cell updates/sec 1 NLVQFGVMIEKMIGKSALQY......YNRKYAHYPNKLCTGPTPPC 123 US-10-088-092A-30\_COPY\_20\_142 - protein search, using sw model Title: Perfect score: OM protein Sequence: Run on:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1276540 seqs, 311283816 residues Searched:

Total number of hits satisfying chosen parameters:

1276540

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:\*

| Cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO7\_NEW PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO6\_NEW PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO7\_NEW PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO7\_NEW PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO0\_PUBCOMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO0\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO0\_NEW\_PUB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Semience 8 Appli	, c	è	325		Semience 1010. An	Sequence 8. Appli	Segmence 3. Appli	. 4	Segmence 7. Appli		3	ì	77	
	ID	US-09-975-456B-8	US-10-255-576-2	US-09-975-456B-6	US-10-205-823-325	US-10-116-275-269	US-09-925-300-1010	US-09-993-999-8	US-10-124-591-3	US-10-124-591-4	US-09-917-805-7	US-09-917-805-6	US-09-917-805-2	US-09-975-456B-2	US-10-104-047-3735	US-10-345-680-23
	DB	101	14	10	14	15	Φ	Q	13	13	12	12	12	10	15	14
	Query Match Length DB	154	124	144	144	144	164	146	146	146	138	138	138	168	168	211
. 040	Query Match	100.0	49.9	49.9	49.9	49.9	49.9	47.2	47.2	46.7	46.5	45.8	43.1	42.0	42.0	42.0
	Score	722	360.5	360.5	360.5	360.5	360.5	341	341	337	335.5	330.5	311.5	303	303	303
	Result No.		73	m	4	Ŋ	9	7	ω	თ	10	11	12	13	14	15

152 PPC 154

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000	equence Sequence Sequence Sequence Sequence	-H-104-10	8, 3, 1, 7, A	Sequence 1, Appl Sequence 1, Appl Sequence 10, Appl Sequence 3518, Ap Sequence 378, App Sequence 534, App Sequence 534, App
15 US-10-295-027-195 16 US-10-275-998-2 16 US-10-188-832-80 19 US-09-987-655-5	0 US-09-975-456 US-09-969-384- 0 US-09-975-456 US-09-835-996A 2 US-10-296-115	-4-7-7	US-09-917-456B US-09-917-456B US-09-917-856B US-09-993-999-7 US-09-993-999-7 US-10-398-68-7	US-10-371-725-7 US-00-993-99-10 US-10-394-33-55 US-09-946-374-37- US-10-147-493-53 US-10-145-127-53
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## ALIGNMENTS

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Sequence 8, Application US/09975456B
| Sequence 8, Application US/09975456B
| GENERAL INFORMATION:
| APPLICANT: LAZDUNSKI, MICHEL
| APPLICANT: LAZDUNSKI, MICHEL
| APPLICANT: LAZDUNSKI, MICHEL
| APPLICANT: LAZDUNSKI, MICHEL
| APPLICANT: VALENTIN, EMMANUEL
| TITLE OF INVENTION: NOVEL NAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
| TITLE OF INVENTION: NOVEL NAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
| TITLE OF INVENTION: NOVEL NAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
| TITLE OF INVENTION: NUMBER: US/09/975,456B
| CURRENT FILING DATE: 2002-08-27
| PRIOR APPLICATION NUMBER: 60/239,491
| PRIOR FILING DATE: 2000-10-11
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NO 8
| LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 KLEXYLESVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 NLVQFGVMIEXMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 722; DB 10; Length 154; 100.0%; Pred. No. 7e-72; 1.ive 0; Mismatches 0; Indels 0.
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Best Local Similarity 100.(
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-09-975-456B-8
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APPLICANT: CLASS AND APPLICANT: CLASS AND APPLICANT: Anderson, Dustin APPLICANT: Anderson, Dustin APPLICANT: Anderson, Dustin TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: THERAPY OF PROSTATE CANCER TITLE OF INVENTION: THERAPY OF PROSTATE CANCER TITLE REPRENCE: MRI-044 CURRENT APPLICATION NUMBER: 60/307,982 CURRENT APPLICATION NUMBER: 60/307,982 PRIOR PILING DATE: 2001-07-25 PRIOR APPLICATION NUMBER: 60/314,356 PRIOR FILING DATE: 2001-08-25 PRIOR PILING DATE: 2001-08-25 PRIOR PILING DATE: 2001-108-25 PRIOR PILING DATE: 2001-108-25 PRIOR PILING DATE: 2001-108-25 PRIOR PILING DATE: 2001-112-12 PRIOR PILING DATE: 2001-12-12 PRIOR PILING DATE: 2001-13-15 PR
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Publication No. US20030211476A1
GAPBICANT Blan Pharacettical Technology
APPLICANT: D'Mahony, Daniel J.
APPLICANT: Brayden, David
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 325, Application US/10205823 Publication No. US20030108963A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gannavarapu, Manjula
Gorbatcheva, Bella
Hoersch, Sebastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
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US-10-205-823-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TPPC 123
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US-10-116-275-269
                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-205-823-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                              Sequence 2, Application US/1025576;
Sequence 2, Application US/1025576;
Publication No. US20030161822A1
GENERAL INFORMATION:
APPLICANT: Weiss, Jercold
APPLICANT: Elang, Ning-Sheng
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
FILE OF INVENTION: ANTIBACTERIAL
CURRENT FILING DATE: 2002-09-25
FILE REFERENCE: 5986/LICATION NUMBER: US/09/740,569
PRIOR PELICATION NUMBER: US 60/172,467
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 5.5
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; Sequence 6, Application No. US20030073087A1
; Sequence 6, Application No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMARNUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REPRENCE: 1479-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; PRIOR APPLICATION NUMBER: 0802-08-27
; PRIOR APPLICATION NUMBER: 60/29,491
; PRIOR PELING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 6
; SEQ ID N
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Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.8%; Pred. No. 5.8e-32;
Matches 68; Conservative 11; Mismatches 44; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-10-255-576-2
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60 PKLEKYLFSVSERGIFC-AGRITCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
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                                                Sequence 8, Application US/0993899
; Sequence 8, Application US/0993899
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: Ho, I-Cheng
; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; TITLE OF INVENTION: Expressed in Th2 Cells
; TITLE OF INVENTION: Expressed in Th2 Cells
; FILE REFERENCE: HUI-O6
; CURRENT APPLICATION NUMBER: US/09/993,999
; FILE REPLICATION NUMBER: 60/246,316
; PRIOR APPLICATION NUMBER: 2000-11-06
; RIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 146;
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CORLEY, Neil C.

NUMBER OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
CCMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.2%; Score 341; DB 9;
52.8%; Pred. No. 9.9e-30;
cive 9; Mismatches 48;
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FLING DATE: «UDKNOWN»
APPLICATION NUMBER: 08/966,317
FILING DATE: «UDKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10124591
Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bandman, Olga
Guegler, Karl J.
Shah, Purvi
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COMPUTER READABLE FORM:
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Best Local Similarity 52.8
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-993-999-8
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US-10-124-591-3
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APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Inelda
TITLE CANT: Higgins Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/2008 CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT APPLICATION NUMBER: US/10/116,275
SURRENT FILING DATE: 2002-10-04
SURMERS OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
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49.9%; Score 360.5; DB 9; Length 164;
Best Local Similarity '55.6%; Pred. No. 7.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1
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Fatent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

ITLE CF INVENTION: Nucleic Acids, Proteins and Antibodies

ITLE REPERENCE: PA101

CURRENT FILING DATE: 2001-08-10

FRIOR FILING DATE: 2000-03-08

FRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PACENTIN VENER: 60/124,270

FRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels
                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-116-275-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-09-925-300-1010
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US-09-925-300-1010
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Gaps

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60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
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.8e-29;
es . 47; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 337; DB 13; Length 146; 50.4%; Pred. No. 2.8e-29;
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Sequence 7, Application US/09917805

Publication No. US20040073973A1

GENERAL INFORMATION:
APPLICANT: STYME, Sten
APPLICANT: STAHL, Ulf
APPLICANT: STAHL, Ulf
APPLICANT: STAME, Ulf
APPLICANT: SJODHEL, Steffan
TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
TITLE REFERENCE: STYME=1
CURRENT FILING DATE: 2001-07-31
FRIOR PLILING DATE: 1999-03-02
PRIOR PRLING DATE: 1999-03-02
PRIOR PLLING DATE: 1997-03-02
PRIOR FILING DATE: 1997-03-02
PRIOR FLING DATE: 1997-03-02
PRIOR FLING DATE: 1997-03-02
PRIOR FLING DATE: 1997-03-02
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PRIOR FLING DATE: 1997-03-02

PRIOR FLING DATE: 1997-03-02

PRIOR FLING DATE: 1997-03-02

PRIOR FLING DATE: 1996-03-03

PRIOR FLING DATE: 1996-03-03
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; Mismatches
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                                                                                                                                                                                                                                  LIBRARY: GenBank
CLONE: 204319
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                    LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.4%
Matches 63; Conservative
                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DISK Comparible
OPERATING SYSTEM: DOS
SOFTWARE: Fast6E0 for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: «UNKNOWN:
APPLICATION NUMBER: US/09/489,770
FILING DATE: «UNKNOWN:
APPLICATION NUMBER: 08/966,317
FILING DATE: «UNKNOWN:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.8%; Pred. No. 9.9e-30;
Matches 66; Conservative 9; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto STATE: CA COUNTRY: USA
                    NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0403 US
TELEPHONE: 650-855-0555
TELEPAX: 650-85-0556
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: 984837
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10124591
Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT Hawkins, Phillip R.
Bandman, Olga
Guegler, Karl J.
Shah, Purvi
                                                                                                                                                                                                                                             LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 KKPKC 146
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US-09-975-456B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 PKTDRYKYHRENGAIVCGKGISCENRICECDRAAAICFRKNLKTYNYIYRNYDDFLCKKE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLVQFGVMIEKMTGKSAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
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Sequence 6, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STYME, Sten
APPLICANT: STAME, U1f
APPLICANT: STAME, U1f
APPLICANT: STODAHL, Staffan
TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
FILE REFERENCE: STYME=1
CURRENT APPLICATION NUMBER: US/09/917,805
CURRENT PILIGATION NUMBER: 09/155,124
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
PRIOR PRILING DATE: 1997-03-27
PRIOR PELING DATE: 1997-03-27
PRIOR PELING DATE: 1997-03-27
PRIOR PELING DATE: 1997-03-27
PRIOR PELING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 14
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| Publication No. US2004007397341
| GENERAL INFORMATION:
| APPLICANT: STYMUE, Sten
| APPLICANT: STAHL, UIF
| TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| FILE REFERENCE: STYMUE=1
| CURRENT APPLICATION NUMBER: US/09/917,805
| CURRENT FILING DATE: 1999-00.73
| PRIOR FILING DATE: 1997-03-27
| PRIOR FILING DATE: 1906-03-29
| NUMBER: OF SEQ ID NOS: 14
| SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.6%; Pred. No. 1.4e-28;
Matches 59; Conservative 18; Mismatches 44;
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; ORGANISM: Trimeresurus flavoviridis
US-09-917-805-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-917-805-6
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US-09-917-805-2
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RESULT 13
US-09-975-456B-2
| US-09-975-456B-3-2
| APPLICANT: LANBEAU, GERARD
| APPLICANT: VALENTIN, ENWANUEL
| TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
| FILE REFERENCE: 1478-R-00
| CURRENT APPLICATION NUMBER: US/09/975,456B
| CURRENT PILING DATE: 2002-08-27
| PRIOR APPLICATION NUMBER: 60/239,491
| PRIOR PILING DATE: 2000-10-11
| WINDER OF SEQ ID NOS: 10
| SEQ ID NO 2: 200-10-11
                                                                                                                                                                                                                                                                                                                                                                                                      61 KLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGIYNR-KYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 PYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMYLCLMNQ--TYREFYRGFLNVYC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 SLINLKAMVEAVTGRSAILSFVGYGCYGGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCH 80
                                                                                                                                                                                                                                                                  18 LWQFENMIIKVVKKSGILSYSAYGCYCGWGGRGKPKDATDRCCFVHDCCYGKV--TGCNP 75
                                                                                                                                                                                                        2 LVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP 60
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                                                                                                              Gaps
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          DB 12; Length 138;
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Sequence 3735, Application US/10104047

Publication No. US20030236392A1

GENERAL INPORMATION:

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REFERENCE: H1-A0105

CURRENT PELING DATE: 2002-03-25

FRIOR FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3735

TYPE: PRI

TYPE:
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43.3%; Pred. No. 1.9e-25;
tive 18; Mismatches 48;
43.1%; Score 311.5; DB 1
50.8%; Pred. No. 1.7e-26;
ive 12; Mismatches 44
Query Match
Best Local Similarity 50.8
Matches 63; Conservative
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Matches 55; Conservative
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ORGANISM: Homo sapiens
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135 SEPC 138
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US-10-104-047-3735
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RESULT 15
US-10-345-680-23
US-10-345-680-23
Sequence 23, Application US/10345680
Sequence 23, Application No. US20030148394A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaccuticals, Inc.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: WEOLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 1230, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPIO2-012PIRNM CMNI
CURRENT APPLICATION NUMBER: US/10/345,680
CURRENT APPLICATION NUMBER: US/10/345,680
                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                      60 PKLEKYLFSV-SERGIFCA--GRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLC 116
                                                                                                                                                                                                                                                                                                                                                                                            60 PKLEKYLFSV-SERGIFCA--GRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLC 116
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                                                                                                                                                                                                                                                         1 NLVQFGVMIBKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                               6; Gaps
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                                                                                      Query Match
42.0%; Score 303; DB 15; Length 168;
Best Local Similarity 43.3%; Pred. No. 1.9e-25;
Matches 55; Conservative 18; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
42.0%; Score 303; DB 14; Length 211;
Best Local Similarity 43.3%; Pred. No. 2.4e-25;
Matches 55; Conservative 18; Mismatches 48; Indels
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PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-02-8

PRIOR PILING DATE: 2002-02-8

PRIOR PILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-04-19

PRIOR PILING DATE: 2002-04-14

PRIOR PILING DATE: 2002-04-14

PRIOR PILING DATE: 2002-04-19

PRIOR PILING DATE: 2002-11-05

PRIOR FILING DATE: 2002-11-05

PRIOR PRIOR PRIING DATE: 2002-11-05

PRIOR PRIEME PRIEMEDATE: 2002-11-26

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 23

LENGTH: 211
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CRGANISM: Homo Sapiens
US-10-345-680-23
; ORGANISM: Homo sapiens
US-10-104-047-3735
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Db 182 QGPTPNC 188

Search completed: July 3, 2004, 05:27:05

Job time : 43.6302 secs
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July 3, 2004, 05:13:08; Search time 25.9925 Seconds (without alignments) 1493.077 Million cell updates/sec
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722
1 NLVQFGVMIEXMTGKSALQY.......YNRKYAHYPNKLCTGFTPPC 123
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_numan:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_nto:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O91v34 rattus norv			OBaxyl bothrops ia						vipera	•		_			c
SUMMARIES	ID	Q91X34	Q7T1D5	Q805A3	Q8AXY1	Q805A2	Q7ZTA8	Q7ZTA6	Q7T1D1	O7T1D4	Q7T1D3	Q7T1D2	Q800C1	O800C2	O7ZTA7	O800C4	Q8N217
	DB	11	13	13	13	13	13	13	13	13	13	13	13	13	13	13	4
	Query Match Length DB	146	138	138	138	138	138	138	138	138	138	138	138	138	138	138	168
æ	Query Match	48.3	46.2	45.1	44.8	44.8	43.7	43.6	43.4	43.3	43.3	43.3	43.0	42.9	42.9	42.3	42.0
	Score	349	333.5	325.5	323.5	323.5	315.5	314.5	313.5	312.5	312.5	312.5	310.5	309.5	309.5	305.5	303
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                                                                                                                                                                                       PKLEKYLFSVSERGIFCA-GRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
                                                                                                                                                                                                                                    82 TKFLIYKFSYRGGRISCSTNQDSCRXQLCQCDKAAAECFARNKKSYSLKYQFYPNKFCKG 141
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                                    59
                                                                                                              22 SLLEFGQMIPFKTGKRADVSYGFYGCHCGVGGRGSPXDATDWCCVTHDCCYNRLEKRGCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22707820; PubMed=12823540;
MEDLINE=22707820; PubMed=12823540;
MEDLINE=22707820; PubMed=12823540;
MIDLIDEMIN I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
"Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom. Identification of the origin of a new viper population pased on
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                                    1 NLVQFGVMIERWIGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ammodytin 11 heterogeneity.";
Bur. J. Bicchem. 270:2897-2706(2003).
EMBL: AYIS8636; AAN59982.1; -
SEQUENCE 138 AA; 15716 MW; 79B9F9E0D16C9CCB CRC64;
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Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase A2.
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Best Local &
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
()(DEL\_TaxID=88087;

[1] SEQUENCE FROM N.A.

Trimeresurus flavoviridis (Habu).

Phospholipase A2. PLA-N.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 PKSDIYSYSWKTGVIICGEGTECEKQICECDRAAAVCFGQNLRTYKKKXMFYPDFLCTDP 134
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EMBL; AY145886; AAN37410.1; GO; GO:0005509; Fighbosholipase A2 activity; IEA.
GO; GO:0004623; Fighbosholipase A2 activity; IEA.
InterPro; IPR001211; PhospholipaseA2.
FighbosholipaseA2.
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MEDLINES-2215-7211; PubMed=12167491;
MEDLINES-2215-7211; PubMed=12167491;
Andriao-Escarso S.H., Soares A.M., Fontes M.R., Fuly A.L.,
Correa F.M., Rosa J.C., Greene L.J., Giglio J.R.;
"Structural and functional characterization of an acidic platelet
"Structural and functional hypotensive phospholipase A(2) from Bothrops
jararacussu snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 NLLQFNKAIKIMTKKNGFPFYTSYGCYCGWGGRGKFKDATDRCCFVHDCCYEKL--TDCS
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TISSUE-Venom gland;
Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLVOFGVMIEKWIGKSALQ-YNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M., Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.; "Interisland mutation of a novel phospholipase A2 from Trimeresurus Flavoviridis venom and evolution of crotalinae group II phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 138;
                                                                                                          Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0004623; F:phospholipase A2 activity; IEA.

R GO; GO:0004623; F:phospholipase A2 activity; IEA.

R GO; GO:0016043; F:phospholipase A2 activity; IEA.

R InterPro; IPR001211; PhospholipaseA2.

R PAINTS; PR00189; PHPHILPASEA2.

R PRINTS; PR00189; PHPHILPASEA2.

R PROSITE; PS00119; PA2 ASP; 1.

R PROSITE; PS00119; PA2 ASP; 1.

R PROSITE; PS00119; PA2 HIS; 1.

R PROSITE; PS00119; PA2 HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       45.1%; Score 325.5; DB 13; Length
49.2%; Pred. No. 1.8e-30;
ative 13; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEWBLrel. 23, Created)
(TrEWBLrel. 23, Last sequence update)
(TrEWBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lochem. Pharmacol. 64:723-732(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Conservative
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Best Local Similarity
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PRELIMINARY;
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         TEKC 138
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                                                                                                                                                                                                                                                                                                                                   Viperidae, Crota.
NCBI_TaxID=8742;
       135
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Chijua T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
"Interisland mutation of a novel phospholipase A2 from Trimeresurus
flavoviridis venom and evolution of crotalinae group II phospholipase
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squama; Chordata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Trimeresurus.
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                                                                                                                                                                Length 138;
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                                                                                                                                                                                                       47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A2.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
              Probon; PD000303; PhospholipaseA2; 1.
SWART; SW00085; PA2c; 1.
PROSITE; PS00118; PA2 AB; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15456 MM; 513647907BFD0F4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q805A2,
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JCN-2003 (TrEMBLrel. 25, Last annotation update)
PLA-N(0).
                                                                                                                                                           44.8%; Score 323.5; DB 13;
46.8%; Pred. No. 3e-30;
ive 16; Mismatches 47;
PR00389; PHPHLIPASEA2
                                                                                                                                                           Query Match
Best Local Similarity 46.8
Matches 58; Conservative
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SEPC 138
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1D 0805A
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60 PKLEKYLFSVSERGIFCAGRITCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
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Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of the venom
                                                                                                                                                                                                                                                                                                                                                                                                          analyses of the venom
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                                                                                                                      Acidic phospholipase A2.

Crotalus viridis (Prairie rattlesnake).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamara; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus
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Crotalus viridis viridis (Prairie rattlesnake).

Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleost
Lepidosauria, Squamata, Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae, Crotalus.
                                                                                                                                                                                                                                                                                                                                                                      TEALLILY. MOSTA, Chen Y.-M., The A.T.;

"Geographic variations, cloning, and functional analyses of acidic phospholipases A2 of Crotalus viridis viridis.";
Arch. Biochem. Biophys. 411:289-296 (2003).

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0016042; F:phospholipase A2 activity; IEA.

R GO; GO:0016042; F:iphic catabolism; IEA.

R PEMPLY PRO0189; P:phipid catabolism; IEA.

R PEMPLY PRO0189; P:phipid catabolism; IEA.

R PALNYS; PR00089; PHPHILPASEA2.

R PRINYS; PR00189; PHPHILPASEA2.

R PROSITE; PS00119; PA2_ASP; 1.

R PROSITE; PS00118; PA2_ASP; 1.

R PROSITE; PS00118; PA2_ASP; 1.

R PROSITE; PS00118; PA2_ASP; 1.
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                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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43.7%; Score 315.5; DB 1
Best Local Similarity 46.0%; Pred. No. 2.7e-29;
Matches 57; Conservative 16; Mismatches 48
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Ammodytin II.
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Q7T1D4;
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Q7T1D3
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                        RESULT 9
Q7T1D4
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Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;

Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;

"Sequences and structural organization of phospholipase A2 genes from

Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom.

Identification of the origin of a new viper population based on

ammodytin II heterogeneity.";

Bur. J. Biochem. 270:2697-2706 (2003).
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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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        Arch. Biochem. Biophys. 411:299-296 (2003).

EMBL; AY120877; AAM80565.1; -...

EMBL; AY120877; AAM80565.1; -...

GO; GO:0004623; F:phospholipase A2 activity; IEA.

GO; GO:0016042; F:phospholipase A2 activity; IEA.

GO; GO:0016042; F:phospholipase A2 activity; IEA.

R FEm. PRO0089; PHPHLIPASEA2.

R PRINTS; PR00189; PHPHLIPASEA2.

R PROSITE; PS00119; PA2. ASF; 1.

R PROSITE; PS00119; PA2. ASF; 1.

R PROSITE; PS00118; PA2. ASF; 1.

S EQUENCE 138 AA; 15440 MW; 44B35FB1EF6B29D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 43.4%; Score 313.5; DB 13; Length Similarity 47.6%; Pred. No. 4.6e-29; S9; Conservative 13; Mismatches 49; Indels
                                                                                                                                                                                                                            Indels
acidic phospholipases A2 of Crotalus viridis viridis.";
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SEQUENCE 138 AA; 15414 MW; 7E8D1EF070880403 CRC64;
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Last annotation update)
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46.0%; Pred. No. 3.5e-29;
tive 16; Mismatches 48;
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                                                                                                                                                                                                                               57; Conservative
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MEDLINE=22707820; 1
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ENLY. A. Biochem. 270:2697-2706 (2003).

ENBL: AXIS9807; AANS9986.1; .. SEQUENCE 138 AA; 15414 MW; C4C985F113EC5DB6 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
                                                                                                                                                                                                       Vipera aspis aspis (Aspic viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euplidosuria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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Pred. No. 6.1e-29;
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15414 MW; C4C985F113EC5DB6 CRC64;
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Last annotation update)
                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q7T1D3;
01-OCT-2003 (TrEMBLrel. 25, C.
01-OCT-2003 (TrEMBLrel. 25, L.
01-OCT-2003 (TrEMBLrel. 25, L.
Ammodytin II isoform 1.
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PRELIMINARY;
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                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=22707820; PubMed=12823540;

Guillemin I. Bouchier C., Garrigues T., Wisner A., Choumet V.;

"Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom. Identification of the origin of a new viper population based on cammodytin II heterogeneity.";

EMEL, J. Biochem. 270:2667-0033.

EMEL, AY159810; AAN598801;
                                                                    1 NLVQFGVMIEKMTG-KSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
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Gaps
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Crotalus viridis (Prairie rattlesnake).
Crotalus viridis viridis (Prairie rattlesnake).
Crotalus viridis viridis (Prairie rattlesnake).
Crotalus viridis Valeostosis (Portebrata, Euteleostomi, Lepidosauria, Macazoa, Clorcoglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Crotalus.
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Vipera.
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; Pred. No. 6.1e-29; 
12; Mismatches 50; Indels 3;
50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59989.1; -. 15414 MW; C4C985F113EC5DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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12; Mismatches
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01-JUN-2003 (TrEMBLrel. 24,
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59; Conservative
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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SEQC 138
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Q800C1;
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OTTID2

ID TO 01-00

DT 01-00

DT 01-00

DE AMMING

ON VIPEL

ON VIPEL

RN NEDLI

RT NEDLI

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0800C1
0800C
AC 0800C
DT 01-JU
DT 01-OC
DT 01-DC
OC Eukar
OC Eukar
OC Viper
OX NGEI
RP SEQUE
Matches
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MEDLINE-22510024; PubMed=12623078;
Teai I.H., Wang Y.M., Chen Y.H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of the venom
action phospholipases A.[2] of Crocalus viridis viridis.";
Arch. Blochem. Blophys. 411:289-296(2003).
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MEDLINE=22510024; PubMed=12623078;
Tsai 1.H., Wang Y.M., Chen Y.H., Tu A.T.;
Geographic variations, cloning, and functional analyses of the venom acidic phospholipases A(2) of Crotalus viridis viridis.";
Arch. Biochem. Biophys. 411:289-296(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SLVÓFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPODATDRCCFVHDCCYGK--ATDCN
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
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Pred. No. 16-28;
...arrhes 50; Indels
                                                                                                                                                                                                                                                         Tsai I.-H., Wang Y.-M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A4403137, AA093140.1; --.
GO; GO:0005609; F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
GO; GO:0016042; F:lipid catabolism; IEA.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHIIPASEA2.
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Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF403134, AA093139.1, -.
GO, GO:0005509; F:calcium ion binding; IEA.
GO, GO:0004623; F:phospholipase A2 activity; IEA.
GO, GO:0016642; P:lipid catabolism; IEA.
InterPro; IPR001211; PhospholipaseA2.
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0-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Les 57; Conservative
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PRINTS; PR00389; PHPHLIPASEA2

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Q800C4
Q800C4;
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MEDLINE=221.0024, PubMed=12623078;

Teal I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;

"Geographic variations, cloning, and functional analyses of the venom acidic phospholipases A2 of Crotalus viridis viridis.";

Arch. Biochem. Blophys. 411:289-296(2003).

R acidic phospholipases A2 of Crotalus viridis.";

Arl20876; AAM80564.1;

R GO; GO:0005609; F:calcium ion binding; IEA.

GO; GO:0016423; P:phospholipase A2 activity; IEA.

GO; GO:0016423; P:phospholipase A2.

InterPro; IPR001211; Phospholipase A2.

R GO; GO:001668; phoslip; 1.

R PRINTS; PR00189; PHPHLPASEA.

R PRINTS; PR00189; PHPHLPASEA.

R SWART; SM00085; PA2c; 1.

R PROSITE; PS00119; PA2_ASS; 1.

R PROSITE; PS00118; PA2_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                    75 PKTVSYTYSVKAGEIICEDDDPCKKQVCECDRVAAVCFRDNIPSYNNNYKRFPAENCRGD 134
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                                                                                                                                                                                                                                                                                                         17 SLVQFEMMIIKVAKRSGLFWYGAYGCYCGWGGQGRPQDATDRCCFVHDCCYGK--AIDCN 74
                                                                                                                                                                                                                                                           1 NLVQFGVMIEKMTGKSAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
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                                                                                                                                                                DB 13; Length 138;
                                                                                                                                                                                                            Indels
               ProDom; PD000303; PhospholipaseA2; 1.
SWART; SW00085; PA2c; 1.
PROSITE; PS00118; PA2_ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15556 MW; 09134B8AB3EE3723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Acidic phospholipase A2.
Crotalus viridis viridis (Prairie rattlesnake).
                                                                                                                                                             42.9%; Score 309.5; DB 13;
46.0%; Pred. No. 1.4e-28;
tive 14; Mismatches 50;
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                                                                                                                                                                                     Local Similarity 46.0%
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les 56; Conserv
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135 PEPC 138

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 PKTVSYTYSEENGEIVCGGDNPCGTQICECDKAAAICFRDNIPSYSNKYWLFLPKNCRGD 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22510024; PubMed=12623078;
Tsal I.H., Wang Y.W., Chen Y.H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of the venom
acidic phospholipases A(2) of Crotalus viridis viridis.";
                                                                                                                                                     Crotalus viridis viridis (Prairie rattlesnake).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trail Test 1.-H., Wang Y.-M.;
Trail 1.-H., Wang Y.-M.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF401134, AA093137.1, -
GO; GO:0004623, F:phospholipase A2 activity; IEA.
GO; GO:0004623, F:lpid catabolism; IEA.
GO; GO:0016042; F:lpid catabolism; IEA.
GO; GO:0016042; F:lpid catabolism; IEA.
InterPro; IPR01211; PhospholipaseA2.
FRINTS; PR00189; PHPHLIPASEA2.
FRODOM: PR00189; PHPHLIPASEA2.
FRODOM: PR00189; PAPHLIPASEA2.
FRODOM: PR00189; PAZ-ASP; 1.
FROSITE; PS00119; PAZ-ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                         01-UNN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th 42.3%; Score 305.5; DB 13; Similarity 46.8%; Pred. No. 4.1e-28; 58; Conservative 12; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arch. Biochem. Biophys. 411:289-296(2003)
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Job time : 25.9925 secs
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Sequence 4, Appli
Sequence 39, Appl
Sequence 39, Appl
Sequence 2, Appli
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                                                                          July 3, 2004, 05:15:00 ; Search time 14.4679 Seconds (without alignments) 506.699 Million cell updates/sec
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                                                                                                                                                         1 MKSPHVLVFLCLLVALVTGN.......YNRKYAHYPNKLCTGPTPPC 142
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Sequence 39,
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Sequence 35,
Sequence 3,
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(GGTZ 6/ptodata/2/iaa/5A_COMB.pep:*

(GGTZ 6/ptodata/2/iaa/5B_COMB.pep:*

(GGTZ 6/ptodata/2/iaa/6A_COMB.pep:*

(GGTZ 6/ptodata/2/iaa/6A_COMB.pep:*

(GGTZ 6/ptodata/2/iaa/6G_COMB.pep:*

(GGTZ 6/ptodata/2/iaa/PCTUS_COMB.pep:*

(GGTZ 6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-170-360-4
US-08-888-497-39
US-09-362-230-39
US-09-740-569-2
PCT-US94-07926-39
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US-09-489-770-3
US-09-489-770-4
US-09-489-770-4
US-09-368-497-42
US-09-362-230-42
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-362-230-37
PCT-US94-07926-37
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US-09-362-230-35
PCT-US94-07926-35
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                                                                                                                                                                                                                            389414 seqs, 51625971 residues
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                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                US-10-088-092A-30
817
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Maximum DB seq length: 200000000
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                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                     Scoring table:
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                                                                           Run on:
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No.
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	ALIGNMENTS					
34,	US-09-362-230-34	4	146	28.3	231.5	<b>4</b> .5
Sequence 34, Appl	-08-888	N	146	28.3	231.5	44
Sequence 4, Appl	US-09-090-602-4		118	29.9	244	
43,	PCT-US94-07926-43		130	35.0	286	42
43,	US-09-362-230-43		130	35.0	286	41
4	US-08-888-497-43		130	35.0	286	
ď	US-09-489-770-1		165	35.2	287.5	
1,	US-08-966-317-1		165	35.2	287.5	
2.5	PCT-US94-07926-22		158	36.2	295.5	37
22,	US-09-362-230-22		158	36.2	295.5	
22,	US-08-888-497-22		158	36.2	295.5	
44,	PCT-US94-07926-44		117	36.3	296.5	
	US-09-362-230-44		117	36.3	296.5	
44	US-08-888-497-44		117	36.3	296.5	32
۲,	US-07-734-534A-1		122	36.7	299.5	31
40,	PCT-US94-07926-40		118	36.7	299.5	30
	US-09-362-230-40		118	36.7	299.5	53
Sequence 5, Appli	US-09-097-094-5		118	36.7	299.5	28

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Length 144;
                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIRET: 1615 L Street, N.W.
CITY: Washington
STRET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PELOFY ALSE
COMPUTER: PASHABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PASHABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: DATORNER: PC-DOS/MS-DOS
SOFTWARE: PASHABLE FORM:
APPLICATION NUMBER: US/08/046,393
FILING DATE: 27-JAN-1994
CLASSIPICATION NUMBER: US/07/810,414
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US/07/810,414
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: US/07/810,414
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
TELEPPAN: 202-202-0944
TELEPPAN: 202-202-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%; Score 368.5; DB 1; 52.1%; Pred. No. 5.1e-32; ive 12; Mismatches 46;
                                                                                                                APPLICANT: Hollis, Melvyn
APPLICANT: Needham, Maurice R.C.
APPLICANT: Needham, Maurice R.C.
APPLICANT: Gooding, Clare
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: Expression Systems
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
                                          Sequence 10, Application US/08186895
Patent No. 5538885
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
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amino acid
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Best Local Similarity 52.1
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-186-895-10
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RESULT 1
US-08-186-895-10
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Gaps

9;

Indels

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Sequence 37, Application US/09362230

Batent No. 6352849

GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide

TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES:

ADDRESSEE: Riden, Barnett, McClosky, Smith, Schuster &

ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
65 VTHDCCYKALEKRGGGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.1%; Pred. No. 5.1e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/097,354
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APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 YNRKYAHYPNKLCTGPTPPC 142
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                                                                                        125 YNKKYQYYSNKHCRGSTPRC 144
                                                                 123 YNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAINES, Peter J.
REGISTRATION NUMBER: 32,264
REFRENCE/POCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 144 amino acids
amino acid
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-09-362-230-37
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                                                                                                         63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRITTCORLICECDKRAALCFRRNLGT 122
                                                                                                                                               65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKODSCRSQLCECDKAAATCFARNKTT 124
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|LILAVIMIFGILQAHGNIVNFHRMIKLTIGKEAALSYGFYGCHCGVGGRGSPKDATDRCC 64
                                                                 64
                               LLVALVT------GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                  12 LLVALVT------GNLVQFGVMIERMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
45.1%; Score 368.5; DB 2;
Best Local Similarity 52.1%; Pred. No. 5.1e-32;
Matches 73; Conservative 12; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/097,354
                                                                                                                                                                                                                               125 YNKKYQYYSNKHCRGSTPRC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: 105-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: US 08/0
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manco, Peter J.
REGISTRATION NUMBER: 32,26
REFERENCE/DOCKET NUMBER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 200 East Browe
CITY: Fort Lauderdale
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305-764-4996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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            GENERAL INFORMATION:

SEQUENCE AL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide

TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Broaded Thereby, Antisense Sequences and Nucleotide

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 HAHDÇÇYGRLEKLGÇEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
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45.1%; Score 368.5; DB 5; Length 144;
Best Local Similarity 52.1%; Pred. No. 5.1e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9
                                                                                                                                                                                                                                                         ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-UUL-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
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US-08-170-360-4
; Sequence 4, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
; APPLICANT: Inglis, Adam
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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7-US94-07926-37
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 PKLEKYLFSVSERGIFCAGRITCORLICECDKRAALCFRRNLGIYNRKYAHYPNKLCTGP 138
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                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floped disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
GUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,360
FILING DATE: 03-WAR-1994
ATTCANEY/AGENT INFORMATION:
APPLICATION NUMBER: AU PK 7058
FILING DATE: G4-JUL-1991
ATTCANEY/AGENT INFORMATION:
NAME: BEINST BATCHER: 30,377
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
RELECOMMUNICATION INFORMATION:
TELEFORM: (202)783-6030
TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS NUMBER OF ESQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: Rothwell, Figg Ernst & Kurz STREET: Suite 701-E, 555 Thirteenth St., N.W STREET: D. C. COUNTRY: D. C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/08888497
Patent No. 5972677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 124 amino acids
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Best Local Similarity
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ANTI-SENSE: N
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US-08-888-497-39
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SEQ ID NO 2
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Sequence 39, Application US/0936230

Retent No. 6322849

GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide

TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: And Antisense Sequences and Nucleotide

STATE: Ruden, Barnett, McClosky, Smith, Schuster & STREET: 200 East Broward Boulevard

CITY: Fort Lauderdale

STREET: 200 East Broward Boulevard

CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 PKLEKYLFSVSERGIFCAGRITCQRITCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.1%; Score 360.5; DB 2; Length 124; 55.6%; Pred. No. 3.1e-31; tive 9; Mismatches 45; Indels 1
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REPERENCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overy Match
Best Local Similarity 55.00
Best Accountable
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-888-497-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 TPPC 142
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STATE: FI
COUNTRY:
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US-09-362-230-39
                                                                                                             COUNTRY:
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APPLICANT: Weiss, Jerrold
APPLICANT: Weiss, Jerrold
APPLICANT: Weiss, Peter
APPLICANT: Liang, Wing-Sheng
APPLICANT: Liang, Wing-Sheng
TITLE OF INVENTION: ANTHRACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
CURRENT APPLICATION NUMBER: US/09/740,569
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/172,467
SPRIOR APPLICATION NUMBER: US 60/172,467
SOFTWARE: PALENT US: 5
SOFTWARE: PALENT US: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 NLVQFGVMIEKWIGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
ZIP: 33301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.1%; Score 360.5; DB 55.6%; Pred. No. 3.1e-31 tive 9; Mismatches 4
                                                                                                                                                                                              PLICASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/898,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING ATE: 26-UL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAISO, PETE. J.
REFERENCE/DOCKET NUMBER: 32.264
REFERENCE/DOCKET NUMBER: 13.264
TELECHONE: 305-764-4956
TELECHAX: 305-764-4956
                                                                                                                                                                                                                                                                                                                                                                                                          IN21044-5
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; Sequence 2, Application US/09740569
; Patent No. 6475484
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 305-/v= ...
INFORMATION FOR SEQ ID NO: 3'
SEQUENCE CHARACTERISTICS:
'TWGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.69
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear / MOLECULE TYPE: protein US-09-362-230-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-569-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 68; Conserv
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 WCCHAHDCCYGRLEKLIGCEPKLEKYLFSVSERGIFCA-GRITCQRLTCECDKRAALCFRR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 WCCVTHDCCYNRLEKRGCGTKFVTYKFSYRGGOISCSTNODSCRKOLCOCDKAAAECFAR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VLVFLCLLVAL-----VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.1%; Score 360.5; DB 2
47.9%; Pred. No. 3.7e-31;
iive 18; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 NKKSYSLKYQFYPNKFCKGKTPSC 146
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                                                                                                                                                                                                  US-08-888-497-35
; Sequence 35, Application US/08888497
• Patent No. 5972677
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FILING DATE: Z6-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAISO, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 amino acids
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Best Local Similarity 47.9
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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CLASSIFICATION:
139 TPPC 142
                                                                121 TPRC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33301
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Sequence 39, Application PC/TUS9407926
Sequence 39, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 Bast Broward Boulevard
CITT: Fort Lauderdale
                                                                                                                                                                                                          79 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 PKLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                1 NLVNFHRLIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG 60
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                          20 NLVQFGVMIEKMIGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEXLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTINUED OF THE CONTINUED OF THE COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPAGE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSITATICATION:
PRIOR APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATPONEY/AGENT INFORMATION:
NAMES TO THE COMPATION:
AND THE COMPATION NUMBER: ADD THE COMPATION:
AND THE COMPATION NUMBER: ADD THE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.1%; Score 360.5; DB 5; 55.6%; Pred. No. 3.1e-31; tive 9; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN21044-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 124 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 55.6
Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                         139 TPPC 142
                                                                                                                                                                                                                                                                                                                                                                             TPRC 124
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PCT-US94-07926-39
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Sequences and Low Molecular Weight Amino Acid Sequences
Encoded Thereby, Antisense Sequences and Nucleotide
Sequences Having Internal Ribosome Binding Sites
    TITLE OF INVENTION: Sequences and Low Molecular Weight Am TITLE OF INVENTION: Encoded Thereby, Antisense Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Bis NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Port Lauderdale
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.1%; Score 360.5; DB 5;
47.9%; Pred. No. 3.7e-31;
tive 18; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REPERBING/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 NLGTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 NKKSYSLKYQFYPNKFCKGKTPSC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHRACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305-764-4996
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Matches 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-966-317-3
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                                                                                                      APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Russell PA
ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 WCCHAHDCCYGRLEKIGCEPKLEKYLFSVSERGIFCA-GRITCORLICECDKRAALCFRR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VLVFLCLLVAL-----VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Sellhamer, Jeffrey J.
TILLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIE: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.1%; Score 360.5; DB 4, 47.9%; Pred. No. 3.7e-31; Itive 18; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE: 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MARSO, PECET J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEPHONE: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 NLGTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                  Sequence 35, Application US/09362230 Patent No. 6352849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.99
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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PCT-US94-07926-35
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60 WCCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCA-GRTTCQRLTCECDKRAALCFRR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
COMPUTER: Thopy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/07926 FILING DATE: 15-JUL-1994 CLASSITCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08966317

Patent No. 6103469

GENERAL INFORMATION:
APPLICANT:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Nail C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
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79 GCGTKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAECFARNKKTYSLKYQFYPNMF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 GCEPKLEKYLPSVSERGIFC-AGRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 VOGNIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGSPKDATDRCCVTHDCCYKSLEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 350; DB 4; Length 146;
Pred. No. 4.9e-30;
9; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08966317;
Sequence 4, Application US/08966317;
Parent No. 6103469;
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceution:
STREBT: 3174 Porton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRATESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Incyte Pharmaceuticals, Inc.
1: 3174 Porter Dr.
Palo Alto
CURRENT APPLICATION DATA:
APPLICATION'NUMBER: US/09/489,770
                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,317
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-0402
TELECOMMUNICATION INFORMATION:
TELEFRENCE 650-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TVDER: amino acids
TVDER: amino acids
TVDER: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.1%;
Matches 68; Conservative
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TTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billings, Lucy J
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 CKGKKPKC 146
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984837
                                                                                                                                                                                                                                                                                                                                                                                                          linear
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TOPOLOGY: lin
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US-09-489-770-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 GCGTKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAECPARNKKTYSLKYQFYPNMF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 VQGNIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGSPKDATDRCCVTHDCCYKSLEKS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEXL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.8%; Score 350; DB 3; Length 146; 53.1%; Pred. No. 4.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: APPLICANT: HUMAN PHOSPHOLIPASE A2 PROTEIN
FOR THE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
FOR THE OF INCYLE, Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
STRATE: CA
                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATURG SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CARRACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-489-770-3
; Sequence 3, Application US/09489770
; Patent No. 6399301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 53.1
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Disket
                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 CTGPTPPC 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: GenB
CLONE: 984837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-966-317-3
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Query Match

42.8%; Score 349.5; DB 3; Length 146;
Best Local Similarity 47.2%; Pred. No. 5.6e-30;
Matches 68; Conservative 18; Mismatches 51; Indels 7.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER:
FLEECOMMUICATION INPORMATION:
TELEPHONE: 650-855-0555
FLEFAX: 650-845-055
FLEFAX: 650-845-055
INPORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
FYPE: amino acid
STRANDEDNESS: single
FOROLOGY: linear
FOROLOGY: linear
FOROLOGY: linear
FOROLOGY: linear
FOROLOGY: linear
FOROLOGY: GenBank
FOROLOGY: GenBank
FOROLOGY: CLONE: 204319
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7; Gaps

Search completed: July 3, 2004, 05:18:46 Job time: 15.4679 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model	July 3, 2004, 05:17:51; Search time 50.3698 Seconds (without alignments) 877.555 Million cell updates/sec
OM protein	Run on:

US-10-088-092A-30 817 1 MKSPHVLVFLCLLVALVTGNVNRKYAHYPNKLCTGPTPPC 142		residues
US-10-088-092A-30 817 1 MKSPHVLVFLCLLVALVTGN	BLOSUM62 Gapop 10.0 , Gapext 0.5	1276540 seqs, 311283816 residues
Title: Perfect score: Sequence:	Scoring table: BLOSUM62 Gapop 10	Searched:

1276540
parameters:
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s satisfying
hits
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number
Total

um DB seq length: 0 um DB seq length: 2000000000 processing: Minimum Match 0% Maximum Match 100 Listing first 45
n DB seq length: n DB seq length: rocessing: Minimu Aaximu Listin
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Minimun Maximun Post-pr

Published_Applications AA:*	1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*	6/ptodata/2/pubpaa/PCT N	6/ptodata/2/pubpaa/US06 NE	6/ptodata/2/pubpaa/US06_PUB	6/ptodata/2/pubpaa/US07	6/ptodata/2/pubpaa/PCTUS PU	6/ptodata/2/pubpaa/US08 NEW PUB.	6/ptodata/2/pubpaa/US08	6/ptodata/2/pubpaa/US09	6/ptodata/2/pubpaa/US09B	6/ptodata/2/pubpaa/US09C	6/ptodata/2/pubpaa/US09	6/ptodata/2/pubpaa/US10A PU	6/ptodata/2/pubpaa/US10B	_6/ptodata/2/pubpaa/US10C_	6/ptodata/2/pubpaa/US10 NEW PUB.	17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*	6/ptodata/2/pubbaa/US60
Database :								<b>1</b> -										

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Seminance R annuit	Segmence 1010. An	Sequence 6. Appl	25. A	69, A	App		App	Appl	App	Appli	App	App		
ion	1 4	100	30e 5	10e 3	ce 2	ce 2	8	1ce 3	ce 7	ce 4	ce 6	ce 2	ce 9	17	7 e 2
Description	1 0	Gueno	egne	Sequence	Sequence 269	Sequence 2.	Sequence 8.	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 17	Sequence 7
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	-456	300-1	-456E	-823-	-275-	-576-	9-666	-591-	-805-	-591-	-805-	-805-	-456E	384-1	-45E
	9-975	-925-	US-09-975-456B-6	0-205	0-116	0-255	-993-	0-124	3-917	)-124	9-917	3-917	9-975	-696-	9-975
ΩI	US-09-975-456B-8	JS-09-925-300-101	US-05	US-1(	US-1	US-10-255-576-2	3-669-669-8L	US-1(	US-09-917-805-7	US-10	US-05	US-05	US-09-975-456B-9	-60-S	US-09-975-456B-7
	101	ָ ני	10	14	15	14	9	13	12	13	12	12	10	0	10
* Query Match Length DB	154	164	144	144	144	124	146	146	138	146	138	138	138	145	145
% Query Match	100.0	45.3	45.1	45.1	45.1	44.1	42.8	42.8	42.8	42.8	42.3	39.8	38.9	38.0	38.0
Score	817	370	368.5	368.5	368.5	360.5	350	350	349.5	349.5	345.5	325.5	317.5	310.5	310.5
Result No.	1 1	7	e	4	ហ	9	7	80	6	10	11	12	13	14	15

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-09-975-456B-	104-047-	345-680-2	295-027-1	275-998	188-832-	35-996A-	296-115	93-999-9	37-655-	37-675-	US-09-975-456	US-10-124-591-	US-09-917-805	US-09-917-805-	US-09-917-805-	US-09-917-805-	US-09-917-	US-09-975-456B	US-09-917-805-	US-09-925-297-5	-666-66-60-SN	US-10-398-6	US-10-290-	US-10-371-7	US-09-946-374-3	10-147-493-53	10-145-127-53	0-160-503-	-10-143-118-53	
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168	168	211	211	211	211	145	150	137	118	118	155	165	145	145	145	145	146	148	148	156	146	151	152	133	116	116	116	116	116	
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16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	ტ ტ	4,0	41	42	43	44	45	

RESULT 1 US-09-975-456B-8 Sequence 8, Application US/09975456B Publication No. US20030073087A1 GENERAL INFORMATION: APPLICANT: LAABLAGUN, GERARD APPLICANT: LAABLAGUN, GERARD APPLICANT: VALENTION: WOVEL NAWMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2 FILE REFERENCE: 1478-R-00 CURRENT APPLICATION NUMBER: US/09/975,456B CURRENT FILING DATE: 2002-08-27 PRIOR PILING DATE: 2000-10-11				100000000000000000000000000000000000000	r rhospholipase az					
RESULT 1 US-09-975-456B-8 Sequence 8, Application US/09975456B Publication No. US2003003087A1 GENERAL INFORMATION: APPLICANT: LAZOUNSKI, MICHEL APPLICANT: LAMBEAU, GERARD APPLICANT: VALENTIN, EWMANUEL TITLE OF INVENTION: NOVEL MAMWALIAN SECRETED GROUP TITLE OF INVENTION NOVEL MAWALIAN SECRETED GROUP CURRENT FILING DATE: 2002-08-27 PRIOR FILING DATE: 2000-10-11 PRIOR FILING DATE: 2000-10-11					1					
RESULT 1 US-09-975-456B-8 Sequence 8, Application US/09975456B Publication No. US20030073087A1 GENERAL INFORMATION: APPLICANT: LAZDUNSKI, MICHEL APPLICANT: LANBEAU, GERARD TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED TITLE REFERENCE: 14708-R-00 CURRENT APPLICATION NUMBER: US/09/975,456B CURRENT FILING DATE: 2002-08-27 PRIOR PILING DATE: 2002-08-27 PRIOR FILING DATE: 2000-10-11				2	GROOF					
RESULT 1 US-09-975-456B-8 Sequence 8, Application US/0997545; Publication No. US20030073087A1 GENERAL INFORMATION: APPLICANT: LAZDUNSKI, MICHEL APPLICANT: LAMBEAU, GERAED APPLICANT: VALENTIN, NOVEL MAMMALI; FILLS REFERENCE: 1478-R-00 CURRENT APPLICATION NUMBER: US/09 CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 2002-08-27 PRIOR FILING DATE: 2002-10-11	Ę	n			AN SECREIED	/975,456B		491		
RESULT 1 US-09-975-456B-8 Sequence 8, Application Publication No. US2003; GENERAL INFORMATION: APPLICANT: LAZDUNSKT, APPLICANT: LAZDUNSKT, APPLICANT: LAZDUNSKT, TITLE OF INVENTION: FILE REFERENCE: 1478- CURRENT APPLICATION N CURRENT APPLICATION N PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE:	2000/011	n 05/099/545 0073087A1	MICHEL	EMMANUEL	R-00	UMBER: US/09	2002-08-27	BER: 60/239,	00-10-11	
RESULT 1 US-09-975-456B. Sequence 8, 7 Sublication 1 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: TITLE OF INF FILE REFEREE CURRENT APPL CURRENT FILE PRIOR APPLIC	8-8-	appications. No. US2003 WATION:	LAMBEAU,	VALENTIN,	VEN 10N: N	LICATION N	ING DATE:	MIN NOT	DATE: 20	
RESOLUTION OF THE STATE OF THE	1 1 9-975-456B	duence o, 1 blication 1 HERAL INFOR	PLICANT: 1	PELICANT:	LE REFEREN	RRENT APPI	RRENT FILL	LIOR APPLIC	LOR FILING	
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ALIGNMENTS

NUMBER OF SEQ ID NOS: 10 SOFTWARE: PatentIn version SEQ ID NO 8 ILENGTH: 154 TYPE: PRT ORGANISM: Homo sapiens US-09-975-456E-8		2.1					
	OF SEQ ID NOS: 10	OFTWARE: Patentin .	EQ ID NO	NGTH: 15	YPE:	RGANISM: Homo sapie	09-975-456B-8

	0;	60	72	120	132
	0; Gaps	VDQTDW	VDQTDW	CFRRNL	CFRRNL
154;		GGSHWP	GGSHWP	DKRAAL	DKRAAL
Length	Indels	YGCYCGI	VGCYCG1	ORLICEC	QRLTCEC
3 10;	0	ALOYNE	ALOYNE	AGRITC	AGRITC
Query Match 100.0%; Score 817; DB 10; Length 154; Best Local Similarity 100.0%; Brad No. 8 ac.82.	Matches 142; Conservative 0; Mismatches 0; Indels	IEKMTGK	13 MKSPHVLVFLCLLVALVTGNLVQFGVMIEXMTGKSALQYNDYGCYCGIGGSHWPVDQTDW 72	61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120	73 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 132
Score	, Mism	ILVOFGVM	LVQFGVM	LEKYLFS	LEKYLFS
0.0%;	, e	'ALVTGN	ALVTGN	LGCEPK	LGCEPK
100	rvativ	FICILIA	FLCLLV	YGRLEK	YGRLEK
nilarit	Conse	SPHVLV	S PHVL	HAHDCC	HAHDCC
tch al Sir	142;	L W	13 MB	61 CC	73 CC
Query Match	tches				
8,6	Σ	ŏ	рр	ò	qq

121 GTYNRKYAHYPNKLCTGPTPPC 142 

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65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
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Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-325
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US-10-116-275-269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 PVDQTDWCCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAA 113
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|LLLAVIMIFGLLQAHGNLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCC 64
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APPLICANT: LAMBEAU, GERARD
APPLICANT: LAMBEAU, GERARD
APPLICANT: VALENTIN, EMMANUEL
TITLE OF INVERTION: NOVEL MANMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
FILE REFERENCE: 1478-R-00
CURRENT APPLICATION NUMBER: US/09/975,456B
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/239,491
PRIOR APPLICATION NUMBER: 60/239,491
PRIOR APPLICATION NUMBER: 60/239,491
RIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 10
SCOTWARE: PatentIn version 2.1
SEQ ID NO 6
LENGTH: 144
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45.1%; Score 368.5; DB 10; Length 144;
Best Local Similarity 52.1%; Pred. No. 1.8e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9;
                                                                        Sequence 1010, Application US/09925300
; Beten No. US20020151681A1
; GENBEAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PACONTIN VET: 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.3%; Score 370; DB 9; Length 164; ilarity 50.3%; Pred. No. 1.5e-32; Conservative 10; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 LCFRRNLGTYNRKYAHYPNKLCTGPTPPC 142
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; Publication No. US20030073087A1
; GENERAL INFORMATION:
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US-09-975-456B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1010
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Best Local Similarity
Matches 75; Conserv
                                                                 -09-925-300-1010
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US-09-975-456B-6
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APPLICANT: ALSO, ALGERIAN AND ANGERIAN APPLICANT: AND TITLE OF INVENTION: METHODS FOR IDENTIFICATIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF PROSTATE CANCER TITLE OF INVENTION: THERAPY OF PROSTATE CANCER FILE REFRENCE: MRI-04
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2002-03-05
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Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
                                                                                                                NESCUL:
US-10-205-823-325
Sequence 325, Application US/10205823
Fublication No. US2030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Bndege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
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125 YNKKYOYYSNKHCRGSTPRC 144
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Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Xumei
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76 GCEPKLEKYLFSVSERGIFC-AGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
RESULT 7
US-09-993-999-8
i Sequence 8, Application US/0993999
j Patent No. US20020110891A1
j CENERAL INFORMATION:
APPLICANT: ATM, JONATHAN P.
APPLICANT: ALSTEN, Frank
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REPERRNCE: HUI-046
CURRENT FILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.8%; Score 350; DB 9; Length 14
Best Local Similarity 53.1%; Pred. No. 2e-30;
Matches 68; Conservative 9; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/489,770
FILING DATE: «Uhknown»
PPLICATION NUMBER: 08/966,317
FILING DATE: «Uhknown»
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Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandman, Olga
Guegler, Karl J.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 146
TYPE: PRT
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US-10-124-591-3
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| Publication No. US20030161822A1
| Sequence 2, Application No. US20030161822A1
| GENERAL INFORMATION:
| APPLICANT: Weiss, Jercold
| APPLICANT: Elsbach, Peter
| APPLICANT: Liang, Ning-Sheng
| TITLE OF INVENTION: AAVIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
| TITLE OF INVENTION: AAVIBACTERIAL
| CURRENT APPLICATION NUMBER: US/10/255,576
| CURRENT APPLICATION NUMBER: US/09/740,569
| PRIOR PAPLICATION NUMBER: US/09/740,569
| PRIOR PILING DATE: 1999-12-17
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 2
| LENGTH: 124
                    APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REPERBNCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 VTHDCCYRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCPARNKKTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LILAVIMIFGLLQAHGNLVNFHRMİKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
44.1%; Score 360.5; DB 14; Length
Best Local Similarity 54.8%; Pred. No. 1.2e-31;
Matches 68; Conservative 11; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                           45.1%; Score 368.5; DB 15; Length
52.1%; Pred. No. 1.8e-32;
ive 12; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 YNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 YNKKYQYYSNKHCRGSTPRC 144
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.1:
Matches 73; Conservative
  Lambkin, Imelda
                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-275-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPRC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-255-576-2
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
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64 DCCYGKL--TNCKPKTDRYSYSRENGVIICGEGTPCEKQICECDKAAAVCFRENLRTYKK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 NKKSYSLKYQFYLNKFCKGKFPSC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                         Sequence 4, Application US/10124591
Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
                                                                                 122 RYMAYPDVLCKKPAEKC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
                                                    126 KYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: 204319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-124-591-4
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US-10-124-591-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GCGTKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAECFARNKKTYSLKYQFYPNWF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 GCEPKLEKYLFSVSERGIFC-AGRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 VQGNIAQFGEMIRLKIGKRAELSYAFYGCHCGLGGKGSPKDATDRCCVTHDCCYKSLEKS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
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42.8%; Score 349.5; DB 12; Length 138;
Best Local Similarity 48.2%; Pred. No. 2.2e-30;
Matches 66; Conservative 15; Mismatches 53; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: STYME, Sten
APPLICANT: STYME, Sten
APPLICANT: STAHL, Ulf
APPLICANT: STAHL, Ulf
APPLICANT: BY-BO
APPLICANT: BY-BO
APPLICANT: BY-BO
APPLICANT: SJODAHL, Staffan
TITLE OF INVENTION: PLANT BNZYME AND USE THEREOF
FILE REFERENCE: STYMNE=1
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 09/155,124
PRIOR APPLICATION NUMBER: 09/155,124
PRIOR APPLICATION NUMBER: 95070554
PRIOR PILING DATE: 1999-03-02
PRIOR PILING DATE: 1997-03-27
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE PATENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
42.8%; Score 350; DB 13;
Best Local Similarity 53.1%; Pred. No. 2e-30;
Matches 68; Conservative 9; Mismatches 49;
                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              LIBEARY: GenBank
CLONE: 984837
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09917805 Publication No. US20040073973A1
              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bothrops jararacussu
US-09-917-805-7
                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 CTGPTPPC 142
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60 WCCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCA-GRITCQRLTCECDKRAALCFRR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 VLVFLCLLVAL-----VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTD 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.8%; Score 349.5; DB 13; Length 146; 47.2%; Pred. No. 2.3e-30; Live 18; Mismatches 51; Indels 7;
COLLEY, Neil C.
COLLEY, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFFWARE: FastERD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-APP-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: CURROWN:
APPLICATION NUMBER: 08/966,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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RESULT 13
US-09-975-456B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.3%; Score 345.5; DB 12; Length Best Local Similarity 46.7%; Pred. No. 5.9e-30; Matches 64; Conservative 21; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OS-09-91/-803-05
| Publication No UG20040073973A1
| GENERAL INFORMATION:
| APPLICANT: STRAIL, UIF
| APPLICANT: STRAINE, SLAIT
| TILLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| TILLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| TILLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| TILLE OF INVENTION: PLANT ENZYME AND USE THEREOF
| FRICK APPLICATION NUMBER: US/09/917,805
| PRIOR PILING DATE: 1999-03-02
| PRIOR FILING DATE: 1999-03-02
| PRIOR FILING DATE: 1997-03-27
| PRIOR FILING DATE: 1996-03-29
| NUMBER OF SEQ ID NOS: 14
| SEQ ID NO 2
| LENGTH: 138
US-09-91/-803-96

US-09-91/-803-96

Publication No. US20040073973A1

GENERAL INFORMATION:

APPLICANT: STYNUE, Sten

APPLICANT: STAHL, Ulf

APPLICANT: STAHL, Ulf

APPLICANT: STOAHL, Staffan

TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF

TITLE REFERENCE: STYNUE:

CURRENT APPLICATION NUMBER: US/09/917,805

CURRENT APPLICATION NUMBER: 09/155,124

PRIOR APPLICATION NUMBER: 09/155,124

PRIOR APPLICATION NUMBER: 99/105,124

PRIOR APPLICATION NUMBER: 99/105,124

PRIOR FILING DATE: 1999-03-02

PRIOR APPLICATION NUMBER: 9601237.2

PRIOR FILING DATE: 1996-03-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE PATENT OF THE PATENT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Trimeresurus flavoviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 IYRNYPDFLCKKESEKC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 KYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-917-805-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-917-805-2
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US-09-969-384-17

Sequence 17, Application US/0969384

Sequence 17, Application No. US20020192749A1

Publication No. US20020192749A1

APPLICANT: Moore, et al.,

ITILE REFERENCE: PT055P1

FILE REFERENCE: PT055P1

CURRENT FILING DATE: 2001-10-03

PRIOR FILING DATE: 2001-10-04-02

PRIOR FILING DATE: 2000-04-02

PRIOR FILING DATE: 2000-09-29

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09975456B
; Sequence 9, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBENU, GERAED
; APPLICANT: LAMBENU, GERAED
; TITLE OF INVENTION: NOVEL MANMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; TITLE OF INVENTION: NOVEL MANMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; TITLE REPERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2000-08-27
; PRIOR PILING DATE: 2000-10-11
; NUMBER: OF SEQ ID NOS: 10
; SOFTWARE: PATENTIN VERSION 2.1
                                                                                                                                                                                                                                                                                           64 DCCYGKV--TGCNPKLGKYTYSWNNGDIVCEGDGPCKEV-CECDRAAAICFRDNLDTYDR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                       66 DCCYGRLEXLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                          7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
                                                                                                                                                                 70 CYGRLEEKGCNIRTQSYKYRFAWGVVTCEPGPPCHVNLCACDRKLVYCLKRNLRSYNPQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 FLACSVPAVQGGLLDLKSMIEKVTGKNALTNYGFYGCYCGWGGRGTPKDGTDWCCWAHDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 CYGRLEKLGCEPKLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKY
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                                                                 2
   39.8%; Score 325.5; DB 12; Length 138; 48.6%; Pred. No. 9.4e-28; tive 15; Mismatches 51; Indels 5;
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45.7%; Pred. No. 7.1e-27;
tive 17; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                              126 -KYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NKYWRYPASNCQEDSEPC 138
Query Match
Best Local Similarity 48.64
Matches 67; Conservative
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Matches 59; Conservative
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130 QYFPNILCS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-4568-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 CCQTHDCCYDHLKTGGCSIXKDYYRYNFSQGNIHCSDKGSWCEQQLCACDXEVAFCLKRN 122
                                                                                                                                                                                                                                                        3 LALLCGLVVMAGVIPIQGGILNLNINYVKQVTGKMPILSYWPYGCHCGLGGRQQPKDATDW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LALLCGLVVMAGVIPIQGGILNLNKAVKQVTGKMPILSYMPYGCHCGLGGRQQPKDATDW 62
                                                                                                                                                                                                                                  7 LVFLCLLVAL-----VTGNLVQFGVMIEXMTGK-SALQYNDYGCYCGIGGSHWPVDQTDW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LANDEAU, MICHEL
APPLICANT: LANDEAU, GERARD
APPLICANT: LANDEAU, GERARD
APPLICANT: VALENTIN, EMANUEL
TITLE OF INVENTION: NOVEL MAWMALIAN SECRETED GROUP IIF PHOSPHOLIPASE AZ
FILE REFERENCE: 1478-R-00
CURRENT APPLICATION NUMBER: US/09/975,456B
CURRENT FILING DATE: 2002-08-27
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VERSION 2.1
SEQ ID NO 7
                                                                                                                                                                                          7; Gaps
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                                                                                                                                                Query Match 38.0%; Score 310.5; DB 9; Length 145; Best Local Similarity 39.2%; Pred. No. 4.5e-26; Matches 56; Conservative 23; Mismatches 57; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                      120 LGTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: July 3, 2004, 05:27:05
Job time : 52.3698 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09975456B Publication No. US20030073087A1 GENERAL INFORMATION:
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 145
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-969-384-17
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Best Local Similarity 39.2%
Matches 56; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-975-4568-7
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US-09-975-456B-7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 3, 2004, 05:12:38; Search time 10.1811 Seconds (without alignments) 726.242 Million cell updates/sec Run on:

US-10-088-092A-30 817 1 MKSPHVLVFLCLLVALVTGN......xNRKYAHYPNKLCTGPTPPC 142 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	criptio	HUMAN	MOUSE 09qul3 mus m		ERIMA P24293 er	HUMAN P14555	A_RAT P14423 rat	ERCE P21789	77y090	TRIFL Q8jig0	P81458	VIPPA	AGKHP 042187	002517	P51972 agki	P31482	P45881	P70088		P00626	P11407	Q8jiy9	P59264	P00622	P06860 t	092147	AGKHP 042188 a	TRIFL P59265	RIMU Q91968	TRIMU Q90w39	AVPO P47711	TRIGA P20476 trimes	CHOC
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P20249 agkistrodon P31854 vinera beru	P18998 crotalus sc P81478 trimeresuru	Q9wvf6 mus musculu P04417 aqkistrodon	Q9pvf2 agkistrodon Q90zz9 echis color	P24294 eristocophi 042192 aqkistrodon	P06859 trimeresuru P81480 trimeresuru
PA22 AGKHA PA2 VIPBB	PA2A CROSS PA22 TRIGA	PA2D_MOUSE PA21_AGKHA	PA2E_AGKRH PA21_ECHCO	PA22_ERIMA PA28_AGKHP	PA21_TRIFL PA23_TRIGA
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122	138	144	139	121	138
40.7	40.7	40.3	40.1	39.8 39.8	39.8
332.5	332.5	329 328.5	328 326.5	325.5	325.5 324.5
3.4	36	3 8 3 8	40	4 4 2	4 4 5 4 5

# ALIGNMENTS

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-!- SIMILARITY: Belongs to the phospholipase A2 family.
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 levels in various other tissues.
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                                                                                                                                     EMBL; AF166098; AAF04499.1; -. EMBL; AF112984; AAF22290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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142 AA;
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PAZN VIPAA ST
AC P34180; 091967;
DT 01-FEB-1994 (Rel.)
DT 16-OCT-2003 (Rel.)
DF 10-OCT-2003 (Rel.)
DF Phospholipase A2,
DE (Phospholipase A2,
CN AMIZ.
OS Vipera ammodytes
OS Ulpera ammodytes
OS Ulpera ammodytes
OS Ulpera ammodytes
OC Eukaryota; Metazes
OC Eukaryota; Metazes
OC Lepidosauria; Squ
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki N., Ishizaki J., Yokota Y.,
Pujii N., Kawamoto K., Hanasaki K.;
Pujii N., Kawamoto K., Hanasaki K.;
Pujii N., Kawamoto K., Hanasaki K.;

"Structures, enzymatic properties, and expression of novel human and
muse secretory phospholipse A(2)";
J. Biol. Chem. 275:5785-5793(2000)
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
--- TALYTIC ACTIVIT: Phosphostholine + H(2)O = 1-
acylg groups in 3-sn-phosphostholine + H(2)O = 1-
acylg groups in 3-sn-phosphostholine + a fatty acid anion.
-!- COFACTOR: Binds I calcium ion per subunit.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower
                                                                                                                                                                                                                                                                                 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE sPLA2) (sPLA2)
PLAAC2E.
                                                                                                                                                                                                                                                        Gaps
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MEDLINE-20002639; PubMed=10531313;
MEDLINE-2. Globmashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
"On the diversity of secreted phospholipases A2. Cloning, tissue distribution, and functional expression of two novel mouse group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(CALCIUM (VIA CARBONYL OXYGEN))
(GY SIMILARITY).
                                                                                                                                                                                                                             Score 817; DB 1; Length 142;
Pred. No. 1e-79;
; Mismatches 0; Indels
                                                                                                                                                      CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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CALCIUM (BY SIMILARITY).
3C360EA710E141FB CRC64;
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                                                                                                                                                                                                                                            Local Similarity 100.0%; Pred. No. 1e-
nes 142; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION. STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 274:31195-31202(1999)
                                                                                                                                                                                                                                                                                                                                                                                  121 GTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                  GTYNRKYAHYPNKLCTGPTPPC 142
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090UL3;
28-FEB-2003 (Rel. 41, Created)
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15989 MW;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase A2, neutral precursor (EC 3.1.1.4) (Ammodytin I2)
(Phosphatidylcholine 2-acylhydrolase).
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Bred. No. 3e-68;
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CALCIUM (BY SIMILARITY).
8B0E3CC710A1F946 CRC64;
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us-10-088-092a-30.rsp

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14; Mismatches
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HSSP; P81458; 1VIP.
InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                  126 KYAHYPNKLCTGPTPPC 142
                                                                                                                                                                  122 KYKNYPSSHCT-ETEQC 137
          73; Conservative
                                                                                                                                                                                                                                                  STANDARD;
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P24293;
01-MAR-1992 (
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                                                                                                                                                                                                                                                                                                   -:-FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
-:-CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion.
-:-COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-:-SUBCELLULAR LOCATION: Secreted.
-:-SUMCALLULAR Belongs to the phospholipase A2 family. Group II
                                                                                                                   "Amino acid and cDNA sequences of a neutral phospholipase A2 from the long-nosed viper (Vipera ammodytes ammodytes) venom."; Eur. J. Biochem. 204:1057-1062(1992).
                                                                                                                                                                                                                                             Kordis D., Gubensek F., "Molecular evolution of phospholipase A2 multigene family in Vipera ammodytes.", Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                               SEQUENCE FROM N.A., AND SEQUENCE OF 17-137.
TISSUE=Venom gland;
MEDLINE=92201190; PubMed=1551386;
Krizaj I., Liang N.-S., Pungercar J., Strukelj B., Ritonja A.,
Gubensek F.;
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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BY SIMILARITY.
                                                                                                                                                                                            Pungercar J.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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BDEC100B7F524431 CRC64;
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PROSITE; PS00118; PA2 HIS; 1.
Hydrolase; Lipid degradation; Calcium; Signal;
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InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHIIPASEA2.
ProDom; PD0003031; PhospholipaseA2; 1.
SMART; SM00085; PA2C; 1.
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EMBL; X84018; CAA58840.1; --
PIR; S22388; S22388.
Viperidae, Viperinae, Vipera.
NCBI_TaxID=8705;
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137 AA;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                             REVISION TO 132.
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SIGNAL
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ACT_SITE
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Best Local Similarity

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                                                          64 DCCYGRVN--GCDPKLSIYSYSFENGDIVCGGDDPCLRAVCECDRVAAICFGENINTYDK 121
                          6 IVAVCLIG--VEGNLYOFGNMIFKMIKKSALLSYSNYGCYCGWGGKGKPQDATDRCCFVH 63
               7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
                                                                                                                                                                                                                                                                                                  DCCYGRLEKLGCEPKLEKYLFSVSERGI FCAGRTTCQRLTCECDXRAALCFRRNLGTYNR
Gaps
                                                                                                                                                                                                                                                           TISSUE=Venom,
MEDLINE=92037623; PubMed=1935962;
Siddiqi A.R., Zaidi Z.H., Joernvall H.;
"Purification and characterization of two highly different group II phospholipase A2 isozymes from a single viperid (Eristocophis
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Viperidae, Viperinae, Eristocophis.
                                                                                                                                                        01-WAR-1992 (Rel. 21, Created)
01-WAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme PLA-1 (EC 3.1.1.4) (Phosphatidylcholine
2-acylhydrolase).
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F5BAA64676954B5E CRC64;
                                                                                                                                           121 AA
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X MEDLINE=2238827; PubMed=12477932;

REDLINE=2238827; PubMed=12477932;

Strausberg R.L., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,

RIAUGHER R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                               79 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 138
                                                                                                                     78
                                                                                                                                                                 28
                                                                                                                   20 NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                   1 NLYQFGKMİFKMIGKSALLSYSDYGCYCGWGGKGKPLDATDRCCFVHDCCYGRVN--GCN
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Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
"Structure and properties of a secretable phospholipase A2 from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89174633; PubMed=2925633;
Kramer R.W., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
Tizard R., Pepinsky R.B.;
"Structure and properties of a human non-pancreatic phospholipase
                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P14555, G9UCD2, 01-727-13, Created) 01-727-1990 (Rel. 13, Created) 01-727-1990 (Rel. 14, Last sequence update) 15-MAR.2004 (Rel. 14, Last annotation update) 15-MAR.2004 (Rel. 14) Last annotation update) Phospholipase A2, membrane associated precursor (BC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2) (GIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2). PLA2G2A OR PLA2B OR RASF-A OR PLA2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIJNE=89174566; PubMed=2925608;
Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
Kloss J., Johnson L.K.;
Kloss J., Johnson L.K.;
Cloning and recombinant expression of phospholipase A2 present in rheumatoid arthritic synovial fluid.";
J. Biol. Chem. 264:5335-5338(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                       Length 121;
                    Query Match
45.5%; Score 372; DB 1; Length 12
Best Local Similarity 56.5%; Pred. No. 1.5e-32;
Matches 70; Conservative 8; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 264:5768-5775(1989).
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SEQUENCE OF 21-54.
TISSUES/TOON-SLAIL HUID;
MEDILINE-89197814; PubMed=3240982;
Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
"Amino acid composition and NRZ-terminal amino acid sequence of human phospholipase A2 purified from rheumatoid synovial fluid.";
J. Biochem. 104:326-328(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Spleen;
MEDLINE-89374261; PubMed=2775276;
Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
"The primary structure of a membrane-associated phospholipase A2 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=55393225; PubMed=7664108;
Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
Billard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich B.D.,
Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
"Structure-based design of the first potent and selective inhibitor
of human non-pancreatic secretory phospholipase A2.";
Nat. Struct. Biol. 2:458-465(1995).
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MEDLINE=91287826; PubMed=2062381;
Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
Marrick M.W., Jones N.D.;
"Structure of recombinant human rheumatoid arthritic synovial fluid
phospholipase A2 at 2.2-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Ileal mucosa;
MEDLINE-3400220; PubMed=8399335;
Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
"Purification and characterization of a phospholipase A2 from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98207049; PubMed=9538252;
Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;
"Crystal structure of human secretory phospholipase A2-IIA complex
with the potent indolizine inhibitor 120-1032.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structures of free and inhibited human secretory phospholipase A2
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lai C.Y., Wada K.;
"Phospholipase A2 from human synovial fluid: purification and structural homology to the placental enzyme.";
Biochem. Biophys. Res. Commun. 157:488-493(1988).
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MEDLINE=92054586; PubMed=1948070;
Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
Sigler P.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 163:42-48(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ileal mucosa.";
Biochim. Biophys. Acta 1170:125-130(1993)
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TISSUE=Synovial fluid;
MEDLINE=89076274; PubMed=3202859;
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Science 254:1007-1010(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human spleen.
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us-10-088-092a-30.rsp

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SEQUENCE FROM N.A.
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   127
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P14423;
                    Query Match
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                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its worlife institutions as long as its content is in no way entities requires a license along the commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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      FUNCTION: Thought to participate in the regulation of the phospholipid metabolism in biomembranes including eicosanoid alosynthesis. Catalyzes the calcium-dependent hydrolysis of the losynthesis. Catalyzes the calcium-dependent hydrolysis of the losynthesis. Catalyzes the calcium-dependent hydrolysis of the losynthic activity. Phosphatidylcholine + H(2)O = 1- acylglycerophosphocholine + a fatty acid anion. COFACTOR: Binds I calcium ion per subunit. SUBCELLULAR LOCATION: Membrane-associated. MISCELLAREQUS: Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene. SIMILARITY: Belongs to the phospholipase A2 family.
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BY SIMILARITY.
BY SIMILARITY.
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(VIA CARBONYL OXYGEN)
(VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                                            GO, GO:0004623; F:phospholipase A2 activity; TAS.
InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; Phoslip 1.
PRINTS; PR00399; PHPHILPASEA2.
ProDom; PD0003039; PhospholipaseA2; 1.
PROSITE; PS000118; PA2_HIS; 1.
PROSITE; PS000119; PA2_ASP; 1.
PROSITE; PS00119; PA2_ASP; 1.
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EMBL; BC05919; AAH05919.1; --
PIR, A32862; PSHUYF.
PDB; 1AYP; 31-JUJ-95.
PDB; 1BC; 31-OCT-93.
PDB; 1POD; 31-OCT-93.
PDB; 1POD; 31-OCT-93.
PDB; 1POF; 31-OCT-93.
PDB; 1POF; 31-OCT-93.
PDB; 1POF; 31-OCT-93.
PDB; 1DB4; 12-NOV-99.
PDB; 1DB4; 12-NOV-99.
PDB; 1DCY; 12-NOV-99.
PDB; 1DCY; 12-NOV-99.
PDB; 1DCY; 12-NOV-99.
PDB; 1DCY; 12-NOV-99.
Biochem. 123:619-623(1998)
                                                                                                                                                                                        EMBL; M22430; AAA36550.1; -.
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                                                                                                                                                                                           64
                                                                                                                                                                    63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGT
                                                                                                                               12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                                      Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=89350908; PubMed=2764915;
Ishizaki J., Chara O., Nakamura E., Tanaki M., Ono T., Kanda A.,
Yoshida N., Teraoka H., Tojo H., Okamoto M.;
"GDNA cloning and sequence determination of rat membrane-associated phospholipase A2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAM-1990 (Rel. 13, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
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STRAIN=Sprague-Dawley; TISSUE=Platelet;
MEDLINE=90110043; PubMed=2606907;
Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;
"Structure of CDNA coding for rat platelet phospholipase A2.";
J. Biochem. 106:545-547 (1989).
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STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=90381322; PubMed=2400792;
Kusunoki C., Satoh S., Kobayashi M., Niwa M.;
"Structure of genomic DNA for rat platelet phospholipase A2.";
Biochim. Biophys, Acta 1087:95-97(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90267443; PubMed=2346480;
Komada M., Kudo I., Inoue K.;
"Structure of gene coding for rat group II phospholipase A2.";
Biochem. Biophys. Res. Commun. 168:1059-1065(1990).
          DB 1; Length 144;
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MEDLINE=89174508; PubMed=3235451;
Mayskawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
Hipe primary structure of rat platelet phospholipase A2.";
J. Biochem. 104:767-772(1988).
                                                                   Indels
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45.1%; Score 368.5; DB 1
52.1%; Pred. No. 4.3e-32;
tive 12; Mismatches 46
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                                                                                                                                                                                                                                                                                                                                                                                    123 YNRKYAHYPNKLCTGPTPPC 142
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Matches 73; Conservative
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Aurolanar P.D., van den Bosch H.;
Immunoaffinity purification, partial sequence, and subcellular
Immunoaffinity purification, partial sequence, and subcellular
Incalization of rat liver phospholipase A2.";
I. J. Biol. Chem. 264:10008-10014 (1989).
C. - FUNCTION: Thought to participate in the regulation of the phospholipid metabolism in biomembranes including eicosanoid biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
C. CATALYTY: Phosphoglycerides.
C. - CATALYTY: Phosphoglycerides.
C. - CATALYTY: Phosphotholine + H (2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
C. - CATALYTY: Binds i calcium ion per subunit (By similarity).
C. - SUBCELLULAR LOCATION: Membrane-associated.
C. - SUBCELLULAR LOCATION: Membrane-associated.
C. - MISCELLANBOUGS: Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene.
C. - SIMILARITY: Belongs to the phospholipase A2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
                                                                                                              MEDIINE=88007474; PubMed=3654593;
Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.;
"Amino acid composition and NH2-terminal amino acid sequence of rat
     Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.; "Purification and characterization of a membrane-associated phospholipase A2 from rat spleen. Its comparison with a cytosolic phospholipase A2 S-1.";
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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SWART; SW00085; PA2c; 1.
PROSITE; PS00118; PA2_HS; 1.
PROSITE; PS00118; PA2_ASP; 1.
Hydrolase; Lipid degrādation; Membrane; Signal; Calcium.
                                                                                                                                                   platelet secretory phospholipase A2.";
J. Biochem. 101:1311-1314(1987).
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Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
                                                            Biol. Chem. 263:5732-5738(1988)
                                                                                                                                                                                                                   MEDLINE=89255484; PubMed=2722857;
 MEDLINE=88186890; PubMed=3356705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D00523; BAA00410.1; --
EMBL; M31127; AAA41223.1; --
EMBL; M25148; AAA41920.1; --
EMBL; X51529; CAA35909.1; --
PIR; A33394; A33394.
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SEQUENCE OF 1-31.
SEQUENCE OF 1-31.
SEQUENCE OF 1-31.
MEDIANCE 90385487; PLEMED 2402760;
Djebari F.L., Martin-Eauclaire M.-F.;
Djebari F.L., Martin-Eauclaire M.-F.;
Djebari F.L., Martin-Eauclaire M.-F.;
Purification and characterization of a phospholipase A2 from "Purification and characterization of a progress cerastes (horn viper) snake venom.";
Toxicon 28:637-646(1990).
-i- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                             63 WCCVTHDCCYNRLEKRGCGTKFLIYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECFAR
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01-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last annoctation update)
10-OCT-2003 (Rel. 42, Last annoctation update)
Cerastes A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
Cerastes cerastes (Horned desert viper).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Wiperidae, Viperinae, Cerastes.
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MEDLINE=91130587; PubMed=1993470;
Siddiqi A.R., Shafqat J., Zaidi Z.H., Joernvall H.;
"Characterization of phospholipase A2 from the venom of Horned viper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                    44.0%; Score 359.5; DB 1; Length 146;
CALCIUM (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                      47.9%; Pred. No. 4e-31; artive 18; Mismatches 50; Indels
                                                                             S -> D (IN REF. 8).
W -> E (IN REF. 5).
R -> S (IN REF. 5).
L -> V (IN REF. 5).
A -> S (IN REF. 5).
A -> S (IN REF. 5).
A -> S (IN REF. 5).
A -> S (IN REF. 5).
                    (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
P -> L (POLYMORPHISM).
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PIR; S13019; S13019.
HSSP; P81458; IVIP.
INTERPRO; IPRO01211; PhospholipaseA2.
Pfam; PP00068; phoslip: 1.
PRINTS; PR00389; PHPHLIPASEA2.
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138 AA.
                                           EMBL; AB072173; BAB66546.1; ...
InterPro; IPR001211; PhospholipaseA2.
PEdan; PF00068; phoslip; 1.
PRINTS; PR00189; PHPHLIPASEA2.
ProDom; PD000103; PhospholipaseA2; 1.
PROSTE; SM01065; PA2c; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium;
                                                                                                                       Calcium;
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138 AA;
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                                                                                                                                                                                                                                                                                         1 NLYQFGKMI FKWIGKSPIFSYGDYGCYCGWGGKGTPVDATDRCCFVHDCCYGRVN--SCN 58
                                                                                                                                                                                                                                                                                                            79 PKLBKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCT 136
                                                                                                                                                                                                                                                                                                                       Gaps
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10-OCT-2003 (Rel. 42, Last annotation update)
Phosphilpase A2 isozyme FL'Y precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase).
Trimeresurus flavoviridis (Habu).
Ebklaryota, Metasca, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Trimeresurus.
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
FKM -> KHK (IN STRAIN TUNISIA).
FIF -> ALL (IN STRAIN TUNISIA).
GD -> SA (IN STRAIN TUNISIA).
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Chijiwa T., Zamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y.,
Hattori S., Ohno M.;
                                                                                                                                                                                                                                  ; Score 358.5; DB 1; Length 120; Pred. No. 4.2e-31; 10; Mismatches 41; Indels 3
                                                                                                                                                                                                                 E6581FA7001C62C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           138 AA
       SMART; SM00085; PA2c; I.
PROSITE; PS00119; PA2 ASP; I.
PROSITE; PS00118; PA2 HIS; I.
Hydrolase; Lipid degradation; Calcium.
ProDom; PD000303; PhospholipaseA2; 1.
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13534 MW;
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120 AA;
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Q90Y77;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme cPLA-B'(A) precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase).
Trimeresurus flavoviridis (Habu).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family; Signal.
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STRAIN=Amami-Oshima, and Kagosima; TISSUE=Venom gland;
MEDLINE=22499762; PubMed=12612832;
Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
Nakashima K.-I., Oda-Ueda N., Pukumaki Y., Hattori S., Ohno M.;
"Interisland evolution of Trimeresurus flavoviridis venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 138;
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PHOSPHLIPASE A2 ISOZYME PL-Y.

PHOSPHLIPASE A2 ISOZYME PL-Y.

BY SIMILARITY.

CALCIUM (VIA CARBONYL OXYGEN)

(BY SIMILARITY).

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Query Match
Best Local Similarity
Matches 66; Conserv
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entiries requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
J. Mol. Evol. 56:286-293(2003).

-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-en-phosphoglycerides.

-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- TISSUE SPECIFICITY: Expressed by the venom gland.

-!- TISSUE SPECIFICITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                  Calcium; Multigene family; Signal.
BY SIMILARITY.
PHOSPHOLIPASE A2 ISOZYME CPLA-B'(A)
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49.2%; Pred. No. 1e-30;
tive 17; Mismatches 47; Indels 3
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CALCUM (NA CARBONYL OXYGEN)
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15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phospholipase Az RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-
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                                                                                                                                                                                                 EMBL; AB087496; BAC02719.1; -.
IINCETPZ; IFR001211; PhospholipaseA2
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHIIPASEA2.
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Conservative 1
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Matches 65; Conserv
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Eaker D., Eklund H.;
acylhydrolase).
Daboja russelli russelli (Russell's viper) (Vipera russelli russe
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBUNIT: Monomer.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Belongs to the phospholipase A2 family. Group II
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InterPro; IRR001211; PhospholipaseA2.
Pfam, PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PA05pholipaseA2; 1.
SWART; SW00085; PA2. 1.
PROSITE; PS00118; PA2. ASP; 1.
PROSITE; PS00118; PA2. HIS; 1.
Hydrolase; Lipid degradation; Calcium; 3D-structure. ACT SITE 47
ACT SITE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13626 MW; 98CBC4A8922A89D1 CRC64;
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53.2%; Pred. No. 9.9e-31;
ive 13; Mismatches 41;
                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                      MEDLINE=98267643; PubMed=9604284;
                                                                           Viperidae, Viperinae, Daboia.
NCBI_TaxID=31159;
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EMBL; AP091884; AAC78084.1; -..

A HSSP; P81458; YUP:

DR PRINTS; PR00121; PhospholipaseA2.

BROOK; PR000303; PhospholipaseA2.

DR PROSTE; P820119; PA2.

TOXAI, Signal; Muligene family.

SIGNAL 17 62 62 BY SIMILARITY.

TOXAI, Signal; Muligene family.

SIGNAL 130 BY SIMILARITY.

104 104 BY SIMILARITY.

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                                   1 NLFQFAEMIVKWIGKNPLSSYSDYGCYCGWGGKGKPQDAIDRCCFVHDCCYEKVK--SCK 58
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Kordis D., Bdolah A., Gubensek F.;

Kordis D., Bdolah A., Gubensek F.;

Kordis D., Bdolah A., Gubensek F.;

Rordis D., Bdolah A., Gubensek F.;

Rordis D., Bdolah A., Gubensek F.;

Biochem. Blophys. Res. Commun. 251:613-619(1998).

-!- FUNCTION: Is not toxic by itself, but the synergistical mixture of vP7 and vP8 is lethal to mice (By similarity).

-!- SUBUNIT: Does not form a complex (By similarity).

-!- SUBCLIULAR LOCATION: Secreted (By similarity).

-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
NLVQFGVMI EXMTGKSAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospholipase A2 homolog VP8 precursor.
Vipera palaestinae (Palestine viper) (Pseudocerastes palaestinae)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                        137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viperidae, Viperinae, Vipera.
NCBI_TaxID=48068;
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                                                                                                                                                                                                                                                                                   64 CCYGTVN--GCDPKLSTYSYSFQNGDIVCGGDDPCLRAVCECDRVAAICFGENMNTYDTK 121
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                                                                                                                            7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHD
                                                                                                                                                                    "Diversity of cDNAs encoding phospholipase A2 from Agkistrodon halys pallas venom, and its expression in B. coli.";
Toxicon 36:1155-1167(1998)
-1-FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2 agyl groups in 3-sn-phosphoglycerides (By similarity).
-1-CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion.
-1-CORACTOR: Binds 1 calcium ion [By similarity).
-1-SUBCELLULAR LOCATION: Secreted (By similarity).
-1-SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan H., Liu X.-L., Ou-Yang L.-L., Yang G.-Z., Zhou Y.-C., Li Z.-P., Wu X.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pāllas).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Gloydius.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoration update)
Phospholipase A2 B precursor (EC 3.1.1.4) (Phosphatidylcholine 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
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PROSITE; PS00118; PA2_HIS; 1.
Lipid degradation; Hydrolase; Signal; Calcium; Multigene family;
                                                                    4;
Length 137;
                                                              40; Indels
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   43.3%; Score 354; DB 1; 54.5%; Pred. No. 1.4e-30; ive 11; Mismatches 40
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Query Match
Best Local Similarity 54.5:
Matches 66; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                    66 DCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRITCORLTCECDKRAALCFRRNLGTYNR 125
                                                                                                                                                                                                                                                                                                                                                                                                    64 DCCYBKL--IGCDPKWDDYTYSWKNGTIVGGDDPCKKEVCECDKAAAICFRDNLKTYKK 121
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A MEDLINE=92409555; PubMed=1528861;
A Kihara H., Odno M.; Nakashima K.-I.; Sasaki H., Hattori M., Sakaki Y., Stihara H., Odno M.;

"Unusually high conservation of untranslated sequences in cDNAs for Trimerseaurus flavoviridis phospholipase A2 isozymes.";

Trimerseaurus flavoviridis phospholipase A2 isozymes.";

Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561(1992).

-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.

-!- CTALLYIC ACTIVITY: Phosphatidylcholine + H(2)O.= 1-acylgycerophosphocholine + a fatty acid anion.

-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SINGLIARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                            LMIVAVLLLGVEGSLLOFRKMIKKMTGKEPVVSYAFYGCYCGSGGRGKPKDATDRCCFVH
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(BY SIMILARITY).
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01-FEB-1994 (Rel. 28, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme PL-X precursor (EC 3.1.1.4)
Phospholipase PL-acylhydrolase)
Trimeresurus flavoviridis (Habu).
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CALCIUM (BY SIMILARITY)
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(See http://www.isb-sib.ch/announce/
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10-UUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Agkistrodon.
                                                               InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00189; PHPHLIPASEA2.
ProDom; PD000103; PhospholipaseA2; 1.
SMART; SM00085; PA2_ASF; 1.
PROSTTE; PS00118; PA2_ASF; 1.
PROSTTE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
SIGNAL
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BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
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CALCIUM (VIA CARBONYL OXYGEN)
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47.4%; Pred. No. 2.6e-30;
iive 18; Mismatches 51
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HSSP; P51972; IVAP.
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WEDLINE=97166209; PubMed=9013608;

Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;

Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;

Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;

The directed mutagenesis study of the phospholipase A2 from the structural aspects of interfacial adsorption. A crystallographic and stre-directed mutagenesis study of the phospholipase A2 from the room of Apristrodon piscivorus P.;

L. J. Biol. Chem. 272:3573-3582(1997).

L. J. Biol. Chem. 273:3573-3582(1997).

L. GATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1- acylglycerophosphocholine + a fatty acid anion.

C. L. CATALYTIC Moreover or homodimer.

S. SUBCELLULAR LOCATION: Secreted.

L. SUBULER LOCATION: Secreted.

C. L. SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                               Cho W., Tomasselli A.G., Heinrikson R.L., Kezdy F.J.;
"The chemical basis for interfacial activation of monomeric
phospholipases A2. Autocatalytic derivatization of the enzyme by acyl
transfer from substrate.";
                                                                                                                                                                                                                                                                 "A new class of phospholipases A2 with lysine in place of aspartate 49. Functional consequences for calcium and substrate binding."; J. Biol. Chem. 259:13839-13843(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR, B53872, 1853872.

PDB; 1VAP; 07-JUL-97.

InterPro; IRPO1211; PhospholipaseA2.

Pfam; PF00058; phoslip; 1.

PRINTS; PR00389; PHPHLIPASEA2.

ProDom; PD000303; PhospholipaseA2; 1.

PROSITE; SW00018; PA2_A5P; 1.

PROSITE; PS00119; PA2_A5P; 1.

PROSITE; PS00118; PA2_A5P; 1.

PROSITE; PS00118; PA2_A5P; 1.
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BEDLINE-85054816; PubMed=6438084;
MATAGANOTE J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,
Heinrikson R.L.;
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N(6)-palmitoyl lysine
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Protein Chem. 12:187-193 (1993).
                                                IISSUE=Venom;
MEDLINE=88298768; PubMed=3403524;
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STRAIN=BALB/C, and CD-1; TISSUB=Intestine;
MEDLINE=95403435; PubMed=7673223.
Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
Ywan M., Tang C., Rancourt D.E., Cromlish W.;
A natural distruption of the secretory group II phospholipase A2 gene
in inbred mouse strains.";
J. Biol. Chem. 270:22378-22385 (1995).
                                                                                                                                                                                                                                                                                                                                                             1 NLFQFEKLIKKMTGKSGMLWYSAYGCYCGWGGQGRPKDATDRCCFVHDCCYGKV--TGCN
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MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,
Buchberg A.M.;
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STRAIN=FVB/N; TISSUE=Colon;
STRAIN=2238025; PubMed=12477932;.
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.482, 066871, 066871, 01.484.

01.401-1993 (Rel. 26, Created)

10.0CT-2003 (Rel. 42, Last sequence update)

15.MAR-2004 (Rel. 43, Last annotation update)

Phospholipase A2, membrane associated precursor (EC 3.1.1.4)

(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)

PLA2G2A.
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NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The secretory phospholipase A2 gene is a candidate for the Momilocus, a major modifier of ApcMin-induced intestinal neoplasia."; Cell 81:957-966(1995).
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                  13989 MW; C39986552D990D72 CRC64;
                                                                                                                                                                                                                                            42.8%; Score 350; DB 1; 52.0%; Pred. No. 3.4e-30; iive 14; Mismatches 42
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PA2A MOUSE
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A Richards S.A., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Small intestine, or 22-41.

WEDLINE-93146172; PubMed-8425615;

MEDLINE-93146172; PubMed-8425615;

MEDLINE-93146172; PubMed-8425615;

MIDHERKAR R., Rao B., Parki V., Chauhan V.S., Deo M.G.;

MIDHORDON R., Rao L., Parki V., Chauhan V.S., Deo M.G.;

The phospholipase A2 family.";

The phospholipase A2 family in the Paneth cells adjacent to the carrier A271 agroups in 3-sn-phospholipase A180 expressed in regenerating liver and hyperplastic esophageal epithelium.

The polymorphism causes a frameshift and premature truncation of the phospholipase A180 expressed in regenerating liver and hyperplastic esophageal epithelium.

The polymorphism causes a frameshift and premature truncation of the protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1, DBA/2, MRL and NZB/BIN contain the normal protein while strain CDATIONAL CANADANISTER.

The pholymorphism causes a frameshift and premature truncation of the protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1, DBA/2, MRL and NZB/BIN contain the normal protein while strain CATALTIONAL CANADANISTER.

The pholymorphism causes a frameshift and premature truncation of the protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1, DBA/2, MRL and NZB/BIN contain the normal protein while strain CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTIONAL CATALTI
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SEQUENCE OF 22-146 FROM N.A.
MEDLINE=94029955; PubMed=8267767;
Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
Mulherkar R. S., wagle A.S., patki V., Deo M.G.;
Enhancing factor, a Paneth cell specific protein from mouse small intestines: predicted amino acid sequence from RT-FCR amplified CDNA
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Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
Blochem. Blophys. Res. Commun. 197:351-352(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and its expression."i Biochem. Biophys. Res. Commun. 195:1254-1263(1993)
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Erratum.
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completed: July 3, 2004, 05:16:39 ne : 10.1811 secs

Search comp Job time :

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EMBL, U32358; AAC52252.1; --EMBL, U38244; AAB06315.1; ALT\_INIT. EMBL; BC045156; AAH45156.1; --FIR; I48342; I48342.

SIMILARITY: Belongs to the phospholipase A2 family.

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76 GCEPKLEKYLFSVSERGIFC-AGRITCORLICECDKRAALCFRRNLGIYNRKYAHYPNKL 134
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                                                                                                                                                     PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
BY SIMILARITY.
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PIR; S29495; S29495.

HSSP; P14555; 1POD.

MGD; MGI:104642; Pla2g2a.

InterPro; IPR001211; PhospholipaseA2.

Pfam; PR00168; PHPHI.PASEAA2.

PRO0189; PR00199; PRAPHI.PASEAA2.

PRODOM; PR00199; PRAPHI.PASEAA2.

PROSTITE; PS00119; PA2 HIS; 1.

PROSTITE; PS00119; PA2 HIS; 1.

PROSTITE; PS00119; PA2—ASP; 1.

Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal; Membrane; Polymorphism.
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(K - > T (IN REF. 1).
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07t1d5 vipera beru

08053 trimeresuru

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07t2d6 crotalus vi

07t2d6 crotalus vi

07t1d1 vipera beru

07t1d3 vipera aspi

07t1d2 vipera aspi

07t1d2 vipera aspi

07t1d2 vipera aspi

07t1d2 vipera aspi

07t1d2 vipera aspi

07t1d3 vipera aspi

07t1d4 vipera espi

080002 crotalus vi

080003 crotalus vi

080004 crotalus vi

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080004 crotalus vi
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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138 138 1438 168 168 168 168 168 168 168 168 168 16		ULT 1  C91934 PRELIMINARY; C91934 D19434 C91934; C1-DEC-2001 (TrEMBLrel. 19, C1-DEC-2001 (TrEMBLrel. 19, C1-OCT-2003 (TrEMBLrel. 25, Platelet phospholipase A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 pratelet A2 propon; PRO01642; Pribid Cat Interer; PRO0164; Pribid Cat Interer; PRO0118; PA2-HIS; SIGNAL 22 A3 prospholipase A	rvative
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SEQUENCE FROM N.A.

TISSUB-Venom gland;

MEDLINE=22157211; PubMed=12167491;

MEDLINE=22157211; PubMed=12167491;

MEDLINE=22157211; PubMed=12167491;

MEDLINE=22157211; PubMed=12167491;

MINTIALO-BECATEO B.H., SOATES A.M., FONTES M.R., Fuly A.L.,

Correa F.M., Ross J.C., Greene L.J., Giglio J.R.;

"Structural and functional characterization of an acidic platelet
aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops
jararacussu snake venom.";

Biochem. Pharmacol. 64:723-732 (2002).
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Franca S.C.;

**Functional and Structural Analysis of Acidic and Basic Phospholipases A2 from Bothrops jararacussus Snake Venom.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AN148985, AN1410.1;

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0006519; F:phospholipase A2 activity; IEA.

GO; GO:0016042; F:lphospholipase A2 activity; IEA.

InterPro; IPR001211; PhospholipaseA2.

PERMI: PF00068; phoslip; 1.
Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M., Oda-Ueda N., Hattori S., Kihra H., Tsunazawa S., Ohno M.; Interistand mutation of a novel phospholipase A2 from Trimeresurus Flavoviridis venom and evolution of crotalinae group II phospholipase
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Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Bothrops.
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A2. ABD102728; BAC56992.1;
CO, GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005602; F:calcium ion binding; IEA.
GO; GO:0006423; F:phospholipase A2 activity; IEA.
GO; GO:0016042; P:lpid catabolism; IEA.
A GO; GO:0016042; P:lpid catabolism; IEA.
A GO; GO:0016042; P:lpid catabolism; IEA.
A FRINTS; PR001021; PhospholipaseA2.
A FroDom; PD000030; PHOSIPASEA2.
A FroDom; PS00103; PAC; I.
A FROSITE; PS00119; PAZ, ASP; I.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.6%; Score 339.5; DB 13;
47.4%; Pred. No. 7.4e-31;
tive 16; Mismatches 53;
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                                   VLVFLCLLVAL-----VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTD
                                                            WCCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCA-GRITCORLICECDKRAALCFRR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Viperinae, Vipera.
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48.8%; Pred. No. 3.4e-31;
Live 14; Mismatches 48; Indels 3;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
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                                                                              DB 13; Length 138;
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                                                                                                   53; Indels
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                             PROSITE; PS00119; PA2 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15456 MW; 513647907BFD0F4E CRC64;
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                                                                           41.3%; Score 337.5; DB 1:
larity 45.3%; Pred. No. 1.3e-30;
Conservative 19; Mismatches 53
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             PhospholipaseA2; 1.
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PROSITE; PS00118; PAZ HIS; 1.
SEQUENCE 138 AA; 15803 MW;
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PRINTS; PR00389; PHPHLIPASEA2
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         ProDom; PD000303; Phosph
SMART; SM00085; PA2c; 1
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"Geographic variations, cloning, and functional analyses of the venom acidic phospholipaes A2 of Crocalus viridis viridis.";

Arch. Blochem. Blophys. 411.289-286(2003).

BMBL, AY120875, AAM80563.1;

GO, GO:0005509; F.-Calcium ion binding; IEA.

GO, GO:0006519; F.-Calcium ion binding; IEA.

GO, GO:001621; F.:phospholipase A2 activity; IEA.

GO, GO:0016623; P::phospholipase A2 activity; IEA.

InterPro; IPR001211; PhospholipaseA2.

PF00068; phoslip; 1.
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MEDLINE=22510024; PubMed=12623078;
TSai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of the venom
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                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Acidic phospholipase A2.
Crotalus viridis viridis (Prairie rattlesnake).
Eukaryota: Metacas, Chorders, Craniata: Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
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45.3%; Pred. No. 8e-30;
tive 18; Mismatches 54; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Acidic phospholipase A2.
Crotalus viridis viridis (Prairie rattlesnake).
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138
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ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HS; 1.
SEQUENCE 138 AA; 15414 MW; 44A35E;
PRT;
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Ammodytin 11.
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Q7T1D4;
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Q7T1D4
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MEDLINE-22707820; PubMed=12823540;
Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
Sequences and structural translation of phospholipase A2 genes from
"Sequences and structural sapis zinnikeri and Vipera berus berus venom."
Identification of the origin of a new viper population based on
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eupidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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                                                                                                                                                                                       40.3%; Score 329.5; DB 13; Length 138; 45.3%; Pred. No. 1e-29; Live 18; Mismatches 54; Indels 3;
acidic phospholipases A2 of Crotalus viridis viridis.";

Arch. Biochem. Biophys. 411:289-296(2003).

Rembl. A120877; AAM805651; -.

GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0016042; P:lipid catabolism; IEA.

R GO; GO:0016042; P:lipid catabolism; IEA.

R InterPro; IPRO1211; PhospholipaseA2.

R Pfam; PR00069; Phoslip; 1.

R PRINTS; PR00389; PHPLIPASEA2.

R ProDom; PR00085; PA2c; 1.

R PROSITE; PS00119; PA2c; 1.

R PROSITE; PS00118; PA2c; 1.

R PROSITE; PS00118; PA2c; 1.

R PROSITE; PS00118; PA2c; 1.
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Bur. J. Biochem. 270:1897-2706(2003).
EMBL; AX189811; AAN18990.1; -
SEQUENCE 138 AA; 15414 MW; 7E8D1EF070880403 CRC64;
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Last annotation update)
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Best Local Similarity 45.3.,
Best Local 62, Conservative
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DCCYGRLEKIGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22707820; PubMed=12823540;
Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
"Sequences and structural organization of phospholipse A2 genes from Vipera agpis, V. aspis zinnikeri and Vipera berus berus venom.
Identification of the origin of a new viper population based on
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Vipera aspis (Aspic viper).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Euplidosuuria; Equamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Viperinae; Vipera.
                                                                                                                        Vipera aspis aspis (Aspic viper).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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46.7%; Pred. No. 1.8e-29;
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46.7%; Pred. No. 1.8e-29;
ive 15; Mismatches 53; Indels
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Bur. J. Biochem. 270:2897-2706(2003).
EMBL, AXIS9808; AANS9887.1; -
ERQUENCE 138 AA, 15414 MW; C4C985F113EC5DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ammodytin 11 heterogeneity.";
Bur. J. Biochem. 270:2697-2706(2003).
EMBL; AXI59807; AAN59986.1; -
SEQUENCE 138 AA; 15414 MW; C4C985F113EC5DB6 CRC64;
25, Created)
25, Last sequence update)
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Q7T1D3;
01-0CT-2003 (TrEMBLrel. 25, C)
01-0CT-2003 (TrEMBLrel. 25, Li
01-0CT-2003 (TrEMBLrel. 25, Li
Ammodytin II isoform 1.
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hes 64; Conservative
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ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
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PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15545 MW;
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Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;

Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;

Sequences and structural organization of phospholipase Az genes from
Vipera aspis aspis. V. aspis zinnikeri and Vipera berus berus venom.

Identification of the origin of a new viper population based on

ammodytin Il heterogeneity.";

Bur. J. Biochem. 270:2697-2706(2003).

EMBL, ANIS9980.1; -.

SEQUENCE 138 AA, 15414 MW; C4C965F113EC5DB6 CRC64;
                                                                                                                  IVAVCLIGA--BGHLSQFGDMINKKTGIFGIMSYIYYGCYCGWGGKGKPLDATDRCCFVH
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      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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Wkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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      53; Indels
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MEDLINE=22510024; PubMed=12623078;
Tsai I.H., Wang Y.M., Chen Y.H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of the venom acidic phospholipases A(2) of Crotalus viridis viridis.";
Arch. Biochem. Biophys. 411:289-296(2003).
                                                                             the venom
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Crotalus viridis (Prairie rattlesnake).
Crotalus viridis viridis (Prairie rattlesnake).
Crotalus viridis viridis (Prairie rattlesnake).
Crotalus viridis viridis (Suraliata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Vineridae; Crotalus.
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MEDLINE=22510024; PubMed=12623078;
Tsai I.H., Wang Y.M., Chen Y.H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of a
acidic phospholipases A(2) of Crotalus viridis viridis.";
Arch. Blochem. Blophys. 411:289-296(2003).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A4403137, AA693140.1;
GO; GO:0005699; F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
GO; GO:0016042; P:lipid catabolism; IEA.
InterPro; IPR01211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR0389; PHPHLIPASEA2.
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MEDLINE 22510024; PubMed=12623078;

Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;

Arch. Biochem. Biophys. 411:289-296(2003).

EMBL, AY120876; AAM80564 11, -.

EMBL, AY120876; AAM80564 11, -.

GO, GO:0004623; F:phospholipase A2 activity; IEA.

GO, GO:0016042; P:lipid catabolism; IEA.

InterProf. IPRO1211; PhospholipaseA2.

Pfromy. PD000189; PHPHLIPASEA2.

Propon PD0001803; PhospholipaseA2; 1.
                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
-Acidic phospholipss A2.
Crotalus viridis viridis (Prairie rattlesnake).
Crotalus viridis viridis (Prairie rattlesnake).
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 43.8%; Pred. No. 8.6e-29;
Matches 60; Conservative 20; Mismatches 54; Indels 3;
                                                                                                DB 13; Length 138;
                                                                                               Query Match .39.4%; Score 321.5; DB 13; Length Best Local Similarity 44.5%; Pred. No. 8.6e-29; Matches 61; Conservative 17; Mismatches 56; Indels
          Prodom; PD000303; PhospholipaseA2; 1.
SMART; SW00085; PA2c; 1.
PROSITE; PS00119; PA2 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15556 MW; 09134B8AB3EE3723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00085; FA2c; 1.
PROSITE; PS001119; PA3 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15549 MW; 04FF6D7266DB0BFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                      138 AA.
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                                                                                                                                                                                                                                                                     126 KYAHYPNKLCTGPTPPC 142
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PRINTS; PR00389; PHPHLIPASEA2
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsai I.H., Wang Y.M., Chen Y.H., Tu A.T.;
"Geographic variations, cloning, and functional analyses of the venom acidic phospholipases A(2) of Crotalus viridis viridis.";
Arch. Biochem. Blophys. 411:289-296(2003).
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                                                                                                                                                                                                                                                                   Crotâlus viridis (Prairie rattlesnake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamaca; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSAIL 1.-H., Wang Y.-M.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF403134; AA093137.1,
CO; GO:0005509; F:calcium ion binding; IEA.
CO; GO:016642; F:lipid catabolism; IEA.
CO; GO:016642; F:lipid catabolism; IEA.
CO; GO:016642; F:lipid catabolism; IEA.
CO; GO:016642; P:lipid catabolism; IEA.
CO; GO:010642; P:lipid catabolism; IEA.
CO; GO:0109; PAC:011;                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
138 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=E6a;
MEDLINE=22510024; PubMed=12623078;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	998.335 Million cell updates/
Title: Perfect score.	US-10-088-092A-30
Sequence:	
Scoring table: BLOSUM62	BLOSUM62
	Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 200000000 DB sed DB sed Minimum I Maximum I

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aab81022 Human pho Abr44235 Human sec	0 0	Aab81021 Murine ph Aab56432 Human pro		PLA2.	Aar63055 Human PLA	2 5	Human	Prosta	Ade63560 Human Pro	Membra		Ada61982 Human G72	Human	Human	8 Rat Pr	983	3 HPLA2-	8 Mouse
SUMMARIES	AAB81022 ABR44235	AB12810	AAB81021 AAB56432	AAP93112 AAP93363	AAR25416	AAR63055 ABR44233	ABP96807	ABU63123	ADB75501	ADE63560 ADA61984	AAR10126	AAW73562	ADA61982	ADA61978	ABR83569	ADE63558	ADA61983	AAR63053	AAW08368
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Length	142	154	1.42	144	144	144	144	144	4.	124	2	124	a	124	124	4	124	145	146
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146 5 ABB08154 125 2 AAK82060 122 3 AAK82060 124 3 AAB12536 144 3 AAB11594 134 2 AAK63046 138 6 ABK4237 138 6 ABK4237 138 7 ADD47915 138 7 ADD47915 138 7 ADD47915 137 7 ADD47913 137 7 ADD47913 137 7 ADD47913 137 7 ADD47913	Abb08154 Murine PL Abp96808 Mouse pho Aar63060 Rat PLA2	Aay88292 Agkistrod Aab12536 Mouse sec Aab11994 Mouse sec	Aar63046 HPLA2-10. Abr44237 Human sec Aae37571 Human pho	Human Human Human	Human Human RPLA2-	Add47917 Rat Prote Add47909 Rat Prote Add47913 Rat Prote Aau09096 Novel hum Abr44234 Hilman sec
200044488888888947777787	ABB08154 ABP96808 AAR63060	AAY88292 AAB12536 AAB11994	AAR63046 ABR44237 AAE37571	ABU63126 ADD47911 ADD47915	ADD47919 AAW58476 AAR63045	ADD47917 ADD47909 ADD47913 AAU09096 ABR44234
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### ALIGNMENTS

Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antiinflammatory; tranquilliser; antiasthmatic; antiallergic; trauma; antirheumatic; antiarthritic; septic shock; pancreatitis; human; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis. Human phospholipase A2 (PLA2) amino acid sequence. AAB81022 standard; protein; 142 AA. (first entry) 12-JUN-2001 AAB81022; RESULT 1 

. .19 |abel= Signal\_peptide Location/Qualifiers Homo sapiens Key Peptide Protein

20. .142 /label= Mature\_PLA2 /note= "Mature\_phospholipase A2" 18-SEP-2000; 2000WO-JP006344. 99JP-00266616. (SHIO ) SHIONOGI & CO LTD. WO200121775-A1 21-SEP-1999; 29-MAR-2001.

Human secretory phospholipase A2 and encoded gene, useful in diagnosis of and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid Χ, Suzuki N, Hanasaki WPI; 2001-290432/30. N-PSDB; AAF77401. Ishizaki J,

Claim 1; Page 46-47; 50pp; Japanese.

arthritis.

This invention relates to human secretory phospholipase A2 (PLA2) protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKBAALCFRRNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120
                                    antibacterial; immunosuppressive; antiinflammatory; tranquilliser; vulnerary; antiasthmatic; antiallergic; antirheumatic; and antiarchritic activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in the diagnosis of PLA2 associated diseases e.g. septic shock, adult respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinitis and rheumatoid arthritis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKWTGKSALQYNDYGCYCGIGGSHWPVDQTDW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group IIF secreted phospholipase A2, sPLA2, phosphatidylglycerol, human, phosphatidylcholine, antibacterial; virucide, cytostatic, vasotropic, antiinflammatory, vulnerary, cardiant, chromosome 1p35, transgenic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR44235

ID ABR44215 standard; protein; 154 AA.

XX AER44215;

XX AER44215;

XX AER44215;

XX TI 18-AUG-2003 (first entry)

XX DT 18-AUG-2003 (first entry)

XX DT 18-AUG-2003 (first entry)

XX DT 18-AUG-2003 (first entry)

XX DT 18-AUG-2003 (first entry)

XX Mocoup IIP secreted phospholipase A2; sPLA2; phosphatidylglycer with the properties of the process of the 
    the gene encoding it. Inhibitors of phospholipase A2 have
                                                                                                                                                                                                                                                                                                                                                                                                            Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 817; DB 4;
100.0%; Pred. No. 1.5e-67;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 142; Conservative
                                                                                                                                                                                                                                                        represents human PLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                    Sequence 142 AA;
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apoptosis is useful for treating disease states or disorders involving group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome or Crohn's disease. Specific antibodies are useful for searching new secreted mammalian group IIF SPLA2 or the homologues of the enzyme in other mammals. The encoding polymucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
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                                                                                                                                                                                                                                                                         Sequences ABR44232-238 represent various human secreted sPLA2 enzymes used in alignment studies with the GIIF sPLA2 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; group IIE secreted phospholipase A2; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, antiinflammatory; vasotropic; cerebroprotective; sPLA2; phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis; viral infection; bacterial infection; cancer; inflammatory disease; cardiac ischaemia; brain ischaemia; acute lung injury; acute respiratory distress syndrome; Crohn's disease; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 817; DB 6; Length 154; 100.0%; Pred. No. 1.6e-67; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human group IIE secreted phospholipase A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GTYNRKYAHYPNKLCTGPTPPC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU63125 standard; protein; 154 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-567302/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 154 AA;
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and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about a 15-fold preference. The mammalian secreted group IIF spLA2 protein or nucleic acid, or a pharmaceutical composition is useful for treating and/or preventing viral infections, bacterial infections, or cancers. The inhibitors of spLA2 or a composition comprising spLA2 inhibitors is useful for treating disease states or disorders involving group IIF sPLA2, e.g. inflammatory disease, cancer, cardiac and brain ischemia, acute lung injury, acute respiratory distress syndrome, or Crohn's compounds for treating these diseases. The amino acid sequence of human group IIE phospholipase A2 used to determine a consensus sequence of thuman spLA2s
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                                                                                                                                                                                                                                                                                                                                                               CCHAHDCCYGRLEKIGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120
                                                                                                                                                                                                                                                                                                                                                                                 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRITCGCREAALCFRRL 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a mouse secretory type phospholipase A2 (PLA2) protein. The mouse secretory type PLA2-like protein can be used for screening in the development of inhibitors against the function of the protein. The present sequence represents mouse secretory type PLA2
                                                                                                                                                                                                                                                                                                                                MKSPHVLVFLCLLVALVTGNLVQFGVMIERMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
                                                                                                                                                                                                                                                                                                      1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                             Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse secretory type phospholipase A2 protein SEQ ID NO:15.
                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                            Score 817; DB 6;
Pred. No. 1.6e-67;
                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             GTYNRKYAHYPNKLCTGPTPPC 142
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                                                                                                                                                                                                                                                                       Matches 142; Conservative
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N-PSDB; AAA73130.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                              Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 142 AA;
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DB 3; Length 142;

Score 709;

86.8%;

Query Match

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                                                                                                              61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNL 120
                                                                                                                                    61 CCHAHDCCYGRLEKLGCDPKLEKYLFSITRDNIFCAGRTACQRHTCECDKRAALCFRHNL 120
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                                                                 Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antiinfiammatory; tranquilliser; antiasthmatic; antiallergic; tranma; antirheumatic; antiatrhritic; septic shock; pancreatitis; mouse; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.
                                              1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
                 Gaps
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0
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                         Murine phospholipase A2 (PLA2) amino acid sequence.
Pred. No. 1.3e-57;
6; Mismatches 16;
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/label= Mature PLA2
/note= "Mature phospholipase A2"
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'label= Signal_peptide
                                                                                                                                                                            121 GTYNRKYAHYPNKLCTGPTPPC 142
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                 Conservative
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Local Similarity
les 120; Conserv
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location/Qualifiers
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22. .37
`--a= "Claim 14"
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/label= exon_1
15. .62
/label= exon_2
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111
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label= signal
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label= exon_3
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88US-00219491.
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/note= "C
                                                                   Local Similarity 50.3
nes 75; Conservative
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                      Sequence 164 AA;
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12-JUL-1988;
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31-JUL-1992
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                                                       Query Match
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, prostate cancer, prostate cancer antigen, detection, diagnosis, neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antilifective, gynaecological, antibacterial, gene therapy, neural, immune, reproductive, renal, gastrointestinal, pulmonary, cardiovascular, proliferative disorder, wound, infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer.
                                                                                                                                                61 CCHAHDCCYGRLEKIGCEPKIEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNL 120
                                                                                                                                                                   61 CCHAHDCCYGRLEKLGCDPKLEKYLFSITRDNIFCAGRTACQRHTCECDRAAALCFRHNL 120
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                                                                                                          1 MKSPHVLVFLCLLVALVTGNLVQFGVMIBKMTGKSALQYNDYGCYCGIGGSHWPVDQTDW
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                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer antigen protein sequence SEQ ID NO:1010.
                          Score 709; DB 4; Length 142; Pred. No. 1.3e-57;
                                                       16; Indels
                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 1443; 2338pp; English
                                                                                                                                                                                                                GTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                AAB56432 standard; protein; 164 AA.
                           86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000WO-US005988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                           Query Match
Best Local Similarity 84.5
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587513/55.
N-PSDB; AAF15635.
Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                         AAB56432;
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2
                                                                                                                                                                                                                                                                                                                                                      76 PKDATDRCCYTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAA 135
                                                                                                                                                                                                                                                                                                                              PVDQTDWCCHAHDCCYGRLEXLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAA 113
                                                                                                                                                                                                                                  4 PHVLVPLCLLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHW 53
                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human inflammatory phospholipase A2 encoded by HindIII fragment of PLA2
8.5 EMBL3.
disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                               16 PRILIMKTLILLAVIMIFGILQAHGNLVNFHRMIKLTIGKEAALSYGFYGCHGGYGGRGS
                                                                                                                                                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inflammation, acid stable; phosphatide 2-acylhydrolase; lipolytic; glycerophospholipids; non-pancreatic.
                                                                                                                                                Length 164;
                                                                                                                                            45.3%; Score 370; DB 3; Length 16
50.3%; Pred. No. 2.6e-26;
ive 10; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44. .56
/note= "calcium binding loop"
                                                                                                                                                                                                                                                                                                                                                                                                                     114 LCFRRNLGTYNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "calcium binding"
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Clone lambda SPLA2cDNA-4 is one of four clones identified when probe oligo 2905 (AAN91257) was used to screen a cDNA library constructed from polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2 type A sequence which is given here. The mature peptide sequence (see FT) has a calculated molecular weight of 13,919 daltons. The same amino acid sequence is also encoded by the exors of clone lambda SPLA2-6 (AANN91260) in Figure 7. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian synovial phospholipase A2 - used in food processing, design screening of inflammation inhibitors, as an anticancer drug or vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LLLAVIMIFGLLQAHGNLVNFHRMIKLTTGKBAALSYGFYGCHCGVGGRGSPKDATDRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human growth hormone; granulocyte-colony stimulating factor; G-CSF; phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy; erythroid cells; cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 45.1%; Score 368.5; DB 1; Length 144; Best Local Similarity 52.1%; Pred. No. 3.2e-26; Matches 73; Conservative 12; Mismatches 46; Indels 9;
                                                                                                                                                                                                                                                                                                                               Seilhamer JJ, Pruzanski W, Vadas P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR25416 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 YNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 YNKKYQYYSNKHCRGSTPRC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 6; 70pp, English.
                                                                                                                                                                                                                                                                            UNIV OF TORONTO INNOVAT
                                                                                                                                    87US-00089883.
88US-00215726.
88US-00231865.
                                                                                       88WO-US002896.
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N-PSDB; AAN91258, AAN91260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adjuvant etc.
                                                                                    23-AUG-1988;
                                                                                                                                          27-AUG-1987;
                                                                                                                                                                   06-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1991;
                                 09-MAR-1989
                                                                                                                                                                                             16-AUG-1988;
                                                                                                                                                                                                                                                                                                                               Johnson LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-1993
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                                                                                                                                                                                                                                                                         UTOR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The protein sequence was deduced from a DNA sequence obtd. from a genomic DNA library which was prepd. from a mutant fibroblast cell line which contains 5 copies of the X chromosome (GMSOD). The signal sequence is thought to be incomplete at the N-terminal since no promoter-like sequences are found in the DNA within 100 nucleo-tides 5' of this region. The deduced N-terminal sequence of the mature protein confirmed results obtd. by direct sequencing of the purified protein. This sequence creatls obtd. by direct sequencing of the purified protein. This sequence represents an amphibilic alpha-helix typical of PLA 2 mols. It has highly conserved lipophilic residues [e.g. Leu (22), Phe (25), and Ile (29)] and there is a cluster of beain amportant determinant in the interaction of PLA 2. There is a characteristic stretch of residues which comprises part of the calcium binding loop: Tyr(44)-G1y-Cys-X-Cys-G1y-C1y-X-X-X-Pro(56) and Asp(68). The conserved residues which constitute the active site (see features) are also present, and the constitute the active site (see features) are also present, and the constitute the active site (see features) are also present, and the constitute the active site (see features) are also present, and the constitute the active site (see features) are also present, and the constitute at the creaminal (The consensus sequence was determined from a comparisom of the consensus proposed to a constitute of the pure of a constitute of the consensus sequence was determined from a comparisom of the consensus sequence was determined from a comparisom of the consensus sequence was determined from a comparisom of the consensus sequence was determined from a comparisom of the consensus sequence was determined from a comparisom of the consensus sequence was determined from a comparisom of the consensus sequence was determined from a comparisom of the consensus sequence was determined to 25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKODSCRSOLCECDKAAATCFARNKTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                    Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LLVALVI-----GNLVQFGVMIEXMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone lambda SPLA2cDNA-4 and by the exons of clone lambda SPLA2-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.1%; Score 368.5; DB 1; Length 144; 52.1%; Pred. No. 3.2e-26; Live 12; Mismatches 46; Indels 9;
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lambda sPLA2-6.
                                                        Hession C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
21. .144
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                                                                                                                                                                                                                                                                 Claim 44; Fig 12; 84pp; English.
                                                                                                                                 N-PSDB; AAN91825, AAN97209
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(first entry)
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nes 73; Conservative
                                                        ĸ,
                                                     Pepinsky
                                                                                                        WPI; 1989-324225/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     correct PR field
(BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 144 AA;
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27-JUN-1980
                                                     Kramer RM,
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Query Match

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AAP93363;

Protein

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122 124

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Gaps . ი

Length 144;

64

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Novel type III and IV low mol. wt. phospholipase A2 enzymes - from humans and rats, also nucleic acid sequences useful, e.g. for recombinant prodn. of enzymes, research into Batten's disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCGCDKRAALCFRRNLGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human; phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic; antinflammatory; vulnerary; cardiant; chromosome 1p35; transgenic;
                                                                                                                                                      A human cDNA (AAQ81138) expressing a novel PLA2, HPLA2-10, was derived from human brain RNA by RACE-PCR. HPLA2-10 (AAR63046) was characterized as a novel type of PLA2, type IV, on the basis of its Cys content in comparison with human PLA2 types I (AAR63054) and II (AAR63055) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a mammalian secreted group IIF secreted phospholipase A2 (sPLA2) (I), where the enzyme is Ca2+ dependent, maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
                                                                                                                                                                                                                                                                                                                                                                                                       GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel mammalian secreted group IIF secreted phospholipase A2, useful preventing and treating bacterial and viral infections, and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted group IIA phospholipase A2 (sPLA2) enzyme.
                                                                                                                                                                                                                                                                                                         bcore 368.5; DB 2;
Pred. No. 3.2e-26;
; Mismatches 46;
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                                                                                                                         Disclosure, Fig 15; 160pp; English
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                                                                                                                                                                                                                                                                                                           45.1%;
52.1%;
vative
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               WPI; 1995-067096/09.
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                                                                                                                                                                                                                                                                                                                                                                                    12 LLVALVT---
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 73; Conser
                                                                                                                                                                                                                                                                            Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003033689-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
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                                                                                                                                                                                                                                                          This sequence is encoded by the phospholipase A2 (PLA2) CDNA. The CDNA was amplified using the primer sequences given in AAQ26370-1 by PCR from a human lung cDNA library. The CDNA sequence was used in the construction of an expression vector which further comprised a promoter and a dominant control region. This vector was used in an expression system comprising a mammalian cell transformed with the vector. This expression system could be used to prepare pharmacologically useful polypeptides eg, human growth hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2, and for gene therapy. The mammalian host comprises erythroid cells and a heterologous promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFAENKIT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                Expression vectors for use in mammalian cells - contain dominant control region derived from beta-globin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 HAHDCCYGRLEKIGCEPKLEKYLPSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 144;
                                                                                              Antonion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.1%; Score 368.5; DB 2;
52.1%; Pred. No. 3.2e-26;
ive 12; Mismatches 46;
                                                                                            Grosveld FG,
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                                                                                                                                                                                                                                             Disclosure; Fig 11; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tischfield JA, Seilhamer JJ;
                                                        (ICIL ) IMPERIAL CHEM IND PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00091941.
93US-00097354.
                       90GB-00027917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INDV ) UNIV INDIANA FOUND. (INCX-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                              Hollis M, Needham MRC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                   WPI; 1992-236158/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PLA2 type II
                                                                                                                                                      N-PSDB; AAQ26372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9502328-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5-JUL-1993;
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                         21-DEC-1990;
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15-AUG-1995
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phosphatidylcholine with a 15-fold preference. A pharmaceutical composition comprising (I) is useful for treating or preventing viral and cancers. A pharmaceutical composition containing capable of inhibiting catalytic activity of (I), biologically active compounds that bind sPLA. receptors, or a compound a population of that modulates cell roliferation, cell migrafion, cell contraction or apoptosis is useful for treating disease states or disorders involving group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain changes a cut clung injury, acute respiratory distress syndrome or changes specific antibodies are useful for searching new secreted mammalian group IIF sPLA2 or the homologues of the enzyme in change and mammals. The encoding polymucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals. Sequences ABR4432-238 represent various human secreted sPLA2 enzymes used in alignment studies with the GIFF sPLA2 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 144 AA;
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63 HAHDCCYGRLEKIGCEPKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGT 122
                                                                                                                                                     65 VTHDCCYRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
                                                                     62
                                                                                                   64
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|LIAVIMIFGLLQAHGNLVNFHRMIKLTTGKBAALSYGFYGCHCGVGGRGSPXDATCC
                                                                 12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
                                     Gaps
                                   <u>ن</u>
   DB 6; Length 144;
                                 46; Indels
45.1%; Score 368.5; DB 6
52.1%; Pred. No. 3.2e-26;
ive 12; Mismatches 46
                                                                                                                                                                                                   YNRKYAHYPNKLCTGPTPPC 142
                                                                                                                                                                                                                                 125 YNKKYOYYSNAHCRGSTPRC 144
                               73; Conservative
Query Match
Best Local Similarity
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                               Matches
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ABP96807 standard; protein; 144 AA (first entry) 05-JUN-2003 ABP96807; RESULT 12 

Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothicate; antinflammatory; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; Human phospholipase A2 group IIA (synovial) SEQ ID NO:3; psoriasis; diabetes; enzyme

Homo sapiens

05-DEC-2002.

WO200297133-A1.

25-MAY-2001; 2001US-00865866.

21-MAY-2002; 2002WO-US016135

(ISIS-) ISIS PHARM INC.

Bennett CF, Wyatt JR;

WPI; 2003-140495/13. N-PSDB; ACC46906, ACC46921.

New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.

Example 13; Page 95-96; 135pp; English.

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The present invention describes a compound (I) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, 2' UTR or intron region of a nucleic acid molecule encoding phospholipase A2 group IIA (synovial), where the compound specifically hybridises with and inhibits the expression of phospholipase A2, group IIA (synovial).

CC Also described: (1) a composition comprising the compound and a carrier or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal hazase or condition associated with phospholipase A2, group IIA (synovial). (1) has antinflammatory, antidiabetic, cytostatic and antipsoriatic activities, and can be used in vaccines and in gene antipsoriatic activities, and can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represente human phospholipase A2 group IIA (synovial), which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKODSCRSOLCECDKAAATCFARNKTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LLLAVIMIFGLLQAHGNLVNFHRMIXLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 144;
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ABU63123
ID ABL65123 standard; protein; 144 AA.
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Human group IIA secreted phospholipase A2. (first entry) 25-SEP-2003 ABU63123;

Human, group IIA secreted phospholipase A2; virucide; antibacterial; cytostatic; antiinflammatory; vasotropic; cerebroprotective; SPLA2; phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis; viral infection; bacterial infection; cancer; inflammatory disease; cardiac ischaemia, brain ischaemia, acute lung injury, acute respiratory distress syndrome, Crohn's disease, enzyme.

Homo sapiens

US2003073087-A1.

17-APR-2003.

11-OCT-2001; 2001US-00975456. 11-OCT-2000; 2000US-0239491P. LAZD/) LAZDUNSKI M. LAMB/) LAMBEAU G. (VALE/) VALENTIN E. 

Valentin E; Lambeau G, Lazdunski M,

WPI; 2003-567302/53.

New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful for treating or preventing viral or bacterial infections, or cancers, or screening inhibitors of the enzyme for treating e.g. inflammatory

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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level of expression of the marker in the patient sample and the normal control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer.

Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB7531 represent marker cDNA and proteins. Note: The sequence of data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the prin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.1%; Score 368.5; DB 7
52.1%; Pred. No. 3.2e-26;
cive 12; Mismatches 46
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                   Disclosure; SEQ ID NO 325; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein P14555, SEQ ID NO 9504.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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GENBANK; P14555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 144 AA;
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                                                                                            The invention describes a mammalian secreted group IIF phospholipase A2 (sPLA2), which is Ca2+-dependent, maximally active at pH of about 7-8, and hydrolyses phosphatidyledline with about a 15-fold preference. The mammalian secreted group IIF sPLA2 protein or mucleic acid, or a pharmaceutical composition is useful for treating and/or preventing viral infections, bacterial infections, or cancers. The inhibitors of splan are composition comprising spla2 inhibitors is useful for treating disease states or disorders involving group IIF sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome, or Crohn's disease. The enzyme is also useful for screening various chemical compounds for treating these diseases. This is the amino acid sequence of them are group IIA phospholipase A2 used to determine a consensus sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
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Anderson D;
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onsey AM, Glatt K, Zhao X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate; cancer; cytostatic; gene therapy; marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          core 368.5; DB 6
red. No. 3.2e-26;
Mismatches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2001US-0307982P.
; 2001US-0314356P.
; 2001US-0325020P.
; 2001US-0341746P.
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For human sPLA2s
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25-SEP-2001;
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RESULT 14 ADB75501

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Length 144; Indels

us-10-088-092a-30.rag

preparing a medicament for treating pain in an animal

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in meuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polynucleotides or their antibodies. The polynucleotide or the compound that compound that compound useful in treating pain and a pharmaceutical composition compound useful in treating pain and apharmaceutical for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CII) and spared nerve injury (MIN) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is patent did not form pair of the printed specification, but was obtained in electronic form directly from wipp at the way obtained in electronic form directly from wipp at the way of the sequences. 

- Sequence 144 AA;

12 LLVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC 62 Query Match

45.1%; Score 368.5; DB 7; Length 144;
Best Local Similarity 52.1%; Pred. No. 3.2e-26;
Matches 73; Conservative 12; Mismatches 46; Indels 9;

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123 YNRKYAHYPNKLCTGPTPPC 142

125 YNKKYQYYSNKHCRGSTPRC 144

Search completed: July 3, 2004, 05:16:16 Job time : 43.1887 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein July 3, 2004, 05:14:29 ; Search time 10.6755 Seconds Run on:

(without alignments)
1108.294 Million cell updates/sec

US-10-088-092A-30\_COPY\_20\_142 Title: Perfect score:

1 NLVQFGVMIEKMTGKSALQY.......YNRKYAHYPNKLCTGPTPPC 123 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

phospholipase A2 (phospholipase escription SUMMARIES \$17860 PSHUYF \$13019 \$22388 B53872 A33394 PSBGAC PSTVXF JC1342 A35493 I50098 I48342 A25806 S10333 JU0283 A33317 S33267 PSVIAA PSVIAC IS1386 IS1190 A44179 PSABA SS9522 S17861 F48188 A37478 I48093 ü Length DB % Query Match 1 Score Result No. 

phospholipase A2 (	phospholipase A2 (	lipase	phospholipase A2 (	phospholipase A2 h	phospholipase A2 (	phospholipase A2 (	phospholipase A2 (	phospholipase A2 (	phospholipase A2 (	phospholipase A2 (	phospholipase A2 h	phospholipase A2 (	phospholipase A2 (	lipase	phospholipase A2 (
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### ALIGNMENTS

RESULT 1  RESULT 1  RESULT 1  RATHEGO DAY 1  STANGO C'Species: Eristocophis macmahoni (leaf-nosed viper)  C'Species: Eristocophis macmahoni (leaf-nosed viper)  C'Species: Day 1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997  C'Accession: S1960  R'Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.  Bur. J. Biochem. 201, 675-679, 1991  ATTITLE: Purification and characterization of two highly different group II phospi  A,Reference number: S17860; MUID:92037623; PMID:1935962  A,Recession: S17860  A,Recule Lype: protein  A,Residues: protein  A,Residues: 1-121 <sid> C'Superfamily: phospholipase A2  C'Keywords: carboxylic ester-hydrolase</sid>	Query Match Best Local Similarity (56.5%;) Pred. No. 5e-29; Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps Qy 1 NLVQFGVMIEKMTGKSA-LQYNDYGCYGGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE Db 1 NLYQFGKMIFKWTGKSA-LLSYSDYGCYCGWGGKGKPLDATDRCCFVHDCCYGRVNGCN	OY 60 PKLEKYLPSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTVRKYAHYPNKLCTGP 119	Qy 120 TPPC 123
31-Oct-1997 int group II pho	4; Gaps 3; YGRLEKLGCE 59    :    YGRVNGCN 58	HYPNKLCTGP 119	

holipase

# PSHUYF

Phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human
NyAlternate names: phosphatidylcholine 2-acylhydrolase; placental PLA2; platelet-secrete
Cispecias: Homo saplens (man)
CiDate: 31-Mar-1993 #text change 15-Sep-2000
CiDate: 31-Mar-1993 #text change 15-Sep-2000
CiDate: 31-Mar-1993 #text change 15-Sep-2000
CiAccession: A32862; B32862; A60266; A32847; A60263; A31350; PT0056; A32913; A60265; A612
Rixtamer, R.M.; Hession, C.; Johansen, B.; Hayes, G.; McGray, P.; Chow, E.P.; Tizard, R.;
A; Feference number: A32862; Mulp:89174633; PMID:2925633
A; Reference number: A32862; Mulp:89174633; PMID:2925633
A; Residues: DNA
A; Residues: 1-144 < kRA>
A; Residues: 1-144 < kRA>
A; Residues: 1-39 < kRA>
A; Residues: 21-39 < kR2>

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phospholipase A2 (EC 3.1.1.4) ammodytin 12 precursor - wes
C;Species: Vipera ammodytes ammodytes (western sand viper)
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A,Molecule type: protein
A,Residues: 1-120 <SID>
C,Superfamily: phospholipase A2
C,Keywords: carboxylic ester hydrolase
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
B; Manda, A; Ono, T; Yoshida, N; Tojo, H; Okamoto, M.
B; Manda, A; Ono, T; Yoshida, N; Tojo, H; Okamoto, M.
B; Mochen B; Ohye. Res. Commun. 163, 42-48, 1989
A; Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
A; Recession: A32913; MUD:89374261; PMID:2775276
A; Recession: A32913; MUD:89374261; PMID:2775276
A; Molecule type: protein
A; Residues: 21-144 - KAN>
R; Parks, T.P.; Lukas, S.; Hoffman, A.F.
Adv. Exp. Med. Biol. 275, 55-81, 1990
A; Title: Purification and characterization of a phospholipase A-2 from human osteoarthrianescence number: A60265; MUD:91050835; PMID:2146857
A; Accession: A60265
A; Molecule type: protein
A; Recklies, A.D.; White, C.
Arthritis Rheum. 34, 1106-1115, 1991
A; Reference number: A61201; MUD:92029121; PMID:1930329
A; Accession: A61201; MUD:92029121; PMID:1930329
A; Accession: A61201; MUD:92029121; PMID:1930329
A;Note: this protein was also detected in platelets
R;Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.
Adv. Exp. Med. Biol. 275, 35-53, 1990
A;Title: Structure and properties of a secretable phospholipase A-2 from human platelets
A;Reference number: A60266; MuID:91050834; PMID:2239446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys., Res. Commun. 157, 488-493, 1988
A;Title: Phospholipase A-2 from human synovial fluid: purification and structural homold
A;Reference number: A31350; MUID:89076274; PMID:3202859
A;Accession: A31350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Refidues: 21-33 cLAI>
R;Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
T. Biochem. 104, 326-328, 1988
A;Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip
A;Reference number: PT0056; MUID:89197814; PMID:3240982
                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-144 «KR3-
A; Residues: 1-144 «KR3-
B; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
G; Biol. Chem. 264, 5335-5338, 1989
A; Pitle: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a A; Reference number: A32847; MUID:89174566; PMID:2925608
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A; Mesidues: 21-40 < REC:
A; Residues: 21-40 < REC:
A; Residues: 21-40 < REC:
A; Experimental source: adult articular cartilage
R; Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott,
Inflammation 15, 355-366, 1991
A; Title: Circulating phospholipase A-2 activity associated with sepsis and septic
A; Reference number: A61634; MUID:92098137; PMID:1757123
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A;Residues: 21-44 <GRES.
A;Residues: 21-74 <GRES.
R;Wery, J. 2. Schevitz,
R;Wery, J. 2. Schevitz,
R;Wery, J. 2. Schevitz,
R;Wery, J. 2. Schevitz,
R;Wery, C.; Warrick, M.W.; Jones, N.D.
Submitted to the Brookhaven Protein Data Bank, May 1992
A;Reference number: A50,Nd3; PDB:1BBC
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: not compared with conceptual translation Nolecule type: mRNA; Residues: 1-144 <CRO>Lai, C.Y.; Wada, K.
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A,Gene: GDB:PLA2G2A; PLA2B; PLA2L
A,Gene: GDB:PLA2G2A; PLA2B; PLA2L
A,Gene: GDB:PLA2G2A; PLA2B; PLA2L
A,Gene: GDB:PLA2G2A; PLA2B; PLA2L
A,Gene: GDB:PLA2G2A; PLA2B; PLA3B; R;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, B.R.; Gamboa, G.; Goodsc Teater, C.; Warrick, M.W.; Jones, N.D.
Mattre 322, 79-82, 1991
A;Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase A;Reference number: A58814; MID:91287826; PMID:2062381
A;Contents: annotation; X-ray crystallography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Cerastes
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C;Species: Cerastes cerastes (horn viper)
C;Date: 19-197 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13019
R;Siddiqi, A.R.; Shafqat, J.; Zaidi, Z.H.; Joernvall, H.
FRBS Lett. 789, 14-16, 1991
A;Title: Characterization of phospholipase A2 from the venom of Horned vipes
A;Reference number: S13019; MUID:91130587; PMID:1993470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG
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ishizaki, J.; Ohara, O.; Nakamura, E.; Tamaki, M.; Ono, T.; Kanda, A.; Yoshida, N.; Tendochem. Biophys. Res. Commun. 162, 1030-1036, 1989
; Jittle: CDNA cloning and sequence determination of rat membrane-associated phospholipase; Reference number: A33394; MCID:89350908; PMID:2764915
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Asticle: Isolation and amino acid sequence of caudoxin, a presynaptic acting toxic phospla. Reference number: A00762; MUID:83042262; PMID:7135414
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                                                                                                                   60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRK-YAHYPNKLCTG 118
                                                                                                                                                                                                         59 PKMDIYTYSVDNGNIVCGCTNPCKKQICECDRAAAICFRDNLKTYDSKTYWKYPKKNCKE 118
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                            1 NLFQFEKLIKKWTGKSGMLWYSAYGCYCGWGGQGRFKDATDRCCFVHDCCYGKV--TGCN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
C;Accession: A33394; JU01111
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C;Species: Bitis caudalis (horned viper)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Apr-1998
C;Accession: A00762
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A; Residues: 1-146 < KOM>
A; Residues: 1-146 < KOM>
A; Cross-references: GB: D00523; NID: g220857; PIDN: BAA00410.1; PID: g220858
C; Superfamily: phospholipase A2
C; Keywords: carboxylic ester hydrolase
F; 1-21/Domain: ajgnal sequence #status predicted < SIG>
F; 22-146/Product: phospholipase A2 #status predicted < MAT>
F; 68,113/Active site: His, Asp #status predicted
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Molecule type: mRNA
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51.2%; Pred. No. 1.6e-26;
iive 14; Mismatches 45
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A.Residues: 1-121 <VIL>
C.Comment: This enzyme is a presynaptic neurotoxin.
C.Function:
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Matches 64; Conserv
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C:Date: 07-Apr-1994 #sequence_revision 19-May-1994 #text_change 21-Jul-2000
C;Accession: S23388; S3686; S36885
R;Krizaj, I.; Liang, N.S.; Pungercar, J.; Strukelj, B.; Ritonja, A.; Gubensek, F.
Eur. J. Blochem. 204, 1057-1062, 1992
A;Title: Amino acid and cDNA sequences of a neutral phospholipase A(2) from the long-nos A;Reference number: S22388; MUD:92201190; PMID:1551386
A;Accession: S2388
A;Molecule type: mRNA
A;Residues: 1-137 <KRI>
A;Accession: S36686
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-137 <KRI>
A;Residues: 17-137 <KRI>
B;Gubensek, F.
Submitted to the EMB1 Data Library, January 1991
A;Residues: 17-137 <KRI>
A;Accession: S3685
A;Accession: S3685
A;Accession: S3685
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C;Species: Agkistrodon piscivorus (cottonmouth)
C;Daces: 26-59p-1994 #sequence_revision 18-Nov-1994 #text_change 24-Jul-1997
C;Accession: B53872
R;Welches, W.; Reardon, I.; Heinrikson, R.L.
J. Protein Chem. 12, 187-193, 1993
A;Title: An examination of structural interactions presumed to be of importance in the eric enzyme from the venom of Agkistrodon p. piscivorus.
A;Reference number: A53872; MUID:93257049; PMID:8489705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 NLYQFGNMIFKMIKKSALLSYSNYGCYCGWGGKGKDQDAIDRCCFVHDCCYGRVN--GCD 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 123;
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A.Molecule type: protein
A.Residues: 1-123 - WELD.
A.Residues: 1-123 - WELD.
A.Roperimental source: venom
A.Note: sequence extracted from NCBI backbone (NCBIP:132046)
C.Superfamily: phospholipase
C.Steywords: carboxylic ester hydrolase
F;47,89/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.5%; Score 350; DB 2;
52.0%; Pred. No. 6.9e-27;
tive 14; Mismatches 42;
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A; Accession: B53872
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Best Local Similarity
Matches 65; Conserve
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A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
C, Function: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A, Mole: the reaction is strongly enhanced when the phospholipid is condensed into a mice
C, Superfamily: phospholipase A2
C, Keywords: calcium; catboxylic ester hydrolase; homodimer; lipid degradation; metallopz
F, 27, 29-44, 41-95, 49-115, 50-88, 57-81, 75-86, Disulfide bonds: #status predicted
F, 27, 29, 31, 48, Binding site: calcium (Tyr, Gly, Gly, Gly, Asp) #status predicted
F, 47, 89/Active site: His, Asp #status predicted
A, Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A,Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C; Superfamily: phospholipase A2 (**Symperfamily: phospholipase A2 (**Symperfamily: phospholipase A2 (**Symperfamily: arboxylic ester hydrolase; lipid degradation; metalloprotein; pres F; 25-121, 27-43, 42-94, 48-149-87, 56-80, 74-85/Disulfide bonds: #status predicted F; 26, 28, 30, 47/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted F; 46, 88/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospholipase A2 (EC 3.1.1.4) X - habu
NyAlternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Accession: A25500
R;Kini, R.M.; Kawabata, S.I.; Iwanaga, S.
Toxicon 24, 1117-1129, 1986
A;Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2
quence of the basic phospholipase, TFV PL-X.
A;Reference number: A94320; MUID:87179112; PMID:3564060
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C;Species: Agkistrodon halys (halys viper)
C;Dacts: 09-0ct-1997 #sequence_revision 07-Nov-1997 #text_change 13-Nov-1998
C;Accession: JC1342
R;Pan, H:; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.
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49.2%; Pred. No. 7.1e-26;
tive 16; Mismatches 44;
                                                                                                                                                                                                            47.1%; Score 340; DB 1;
47.2%; Pred. No. 6.3e-26;
tive 15; Mismatches 48
                                                                                                                                                                                                                                       Similarity 47.2% S8; Conservative
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Matches 61;
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Best Local 9
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A,Accession: JC1342
A,Molecule type: mRNA
A,Residues: 1-138 PANA
A,Residues: 1-138
A,Note: unthors translated the codon GAC for residue 54 as Asn
C,Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of 3-C;Superfamily: phospholipase A2
C;Superfamily: phospholipase A2
C;Superfamily: phospholipase A2
F;1-16,Domain: signal sequence #status predicted <SIG>
F;11-138/Product: phospholipase A2 #status predicted <MAT>
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A; Cross-references: EMBL:X51529; NID:g56930; PIDN:CAA35909.1; PID:g56931
R; Aarsman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch, Arch. Biochem. Biophys. 331, 95-103, 1996
A; Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from 1A; Reference number: S71310; MUID:96268465; PMID:8660688
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Astacle type: DNB
Biochim. Biophys. Acta 1087, 95-97, 1990
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 14-Sep-1990 #sequence revision 18-Nov-1992 #text_change 18-Ju
Cispecession: A35493, 13188; 371310
Eiochem. Biophys. Res. Commun. 168, 1059-1065, 1990
A; Tille: Structure of gene coding for rat group II phospholipase A-2. A; Reference number: A35493; MUID:90267443; PMID:2346480
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Acta Biochim. Biophys. Sin. 28, 579-582, 1996
A;Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas.
A;Reference number: JC1342
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A,Molecule type: protein
A,Reducus: 22-29, /x', 31-32, /x', 34 <AAR>
A,Experimental source: kidney
C,Superfamily: phospholipase A2
C,Keywords: carboxylic ester hydrolase; lipid degradation
F,68,113/Active site: His, Asp #status predicted
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Pred. No. 1.4e-25;
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50.0%; Pred. No. 7.9e-26;
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tive 14; Mismatches
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Matches 63; Conservative
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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                         A; Contents: Snake venom
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A/Accession: S35948
A/Molecule type: mRNA
A/Residues: 22-115.78',118-146 <MUL3>
A/Cross-references: EMBL:X74266
B/Cross-references: EMBL:X74258
B/Cross-references: EMBL:X74258
B/Cross-references: EMBL:X7258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 PKTDRYKYHRENGAIVGKGKGTSCENRICECDRAAAICFRKNLKTYNHIYMYYPDFLCKKE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phospholipase A2 (EC 3.1.1.4) B - western sand viper NiAlternate names: ammodytoxin B C;Species: vipera ammodytes ammodytes (western sand viper) C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 28-Aug-1998 C;Accession: A25806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 NIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGSPKDATDRCCVTHDCCYKSLEKSGCG
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47.6%; Pred. No. 2.7e-25;
ive 18; Mismatches 44.
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Keywords: carboxylic ester hydrolase
68,113/Active site: His, Asp #status predicted
                  submitted to the EMBL Data Library, July 1993
A;Reference number: S35948
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Best Local Similarity 47.6%
Matches 59; Conservative
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C;Species: Wus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148342; PC2009; S35948; 149352
R;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A;Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: p.A;Accession: 148342
A;Accession: 148342
A;Accession: Laye: mRD:
A;Accession: Laye: mRD:
A;Accession: Laye: mRD:
A;Molecule Vype: mRD:
A;Molecule Cype: mRD:
A;Molecule Cype: mRD:
A;Residues: 1-146 cMUL.
A;Cross-references: EMBL:X74266; NID:9557247; PIDN:CAA52325.1; PID:9557248
R;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A;Title: Enhancing factor, a peneth cell specific protein from mouse small intestines: p.A;Accession. Decomm. P.A;Accession. P.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISO098
phospholipase a2 - jararacussu
C;Species: Dothrops jararacussu (jararacussu)
C;Species: Dothrops jararacussu (jararacussu)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C;Accession: ISO098; S44247
C;Accession: ISO098; S44247
C;Accession: ISO098; S44247
C;Accession: 150098; MUID:95395872; PMID:7665446
A;Title: The molecular cloning of a phospholipase A2 from Bothrops jararacussu snake ver
A;Reference number: ISO098; MUID:95395872; PMID:7665446
A;Accession: ISO098
                                                                                                                                                                                    PKLEKYLFSVSERGIFCA-GRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
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                                                      81
SLLEFGOMILFKTGKRADVSYGFYGCHCGVGGRGSPKDATDMCCVTHDCCYNRLEKRGCG
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C;Genetics:
C;Genetics:
C;Superfamily: phospholipase A2
C;Superfamily: phospholipase A2
F;63,105/Active site: His, Asp #status predicted
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A;Note: correction of S35948
R;Mulherkar, R:; Rao, R:; Wagle, A:; Patki, V:; Deo, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.5%; Score 335.5; DB 2
50.0%; Pred. No. 1.9e-25;
iive 12; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-138 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         119 PTPPC 123
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14 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PKLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 PKTDRYKYHRENGAIVCGKGTSCENRICECDRAAAICFRKNLKTYNHIYMYYPDFLCKKE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLVQFGVMIEKWTGKSAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLVQFGVMIERMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
ammödytoxin B precursor – sand viper
C;Species: Vipera ammodytes (sand viper)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C.Species: Rattus norvegicus (Norway rat)
C.Jate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
C.Accession: JU0283
                                                                                                                                                                                                                                                                                                                                                                                                                        17 SLLEFGMMILGETGKNPLISYSFYGCYCGVGGKGTPKDATDRCCFVHDCCYGNLP--DCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                      R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K. J. Biochem. 106, 545-547, 1989
A;Title: Structure of cDNA coding for rat platelet phospholipase A2. A;Reference number: JU0131; MUID:90110043; PMID:2606907
A;Accession: JU0283
                                                                                                                                                                                                                                                                                                           Query Match

46.2%; Score 333.5; DB 2; Length 138;
Best Local Similarity 47.6%; Pred. No. 3e-25;
Matches 59; Conservative 18; Mismatches 44; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: mRNA

A, Residues: 1-146 < KKOM>

C, Superfamily: phospholipase A2

C, Keywords: carboxylic ester hydrolase

F,1-21/Domain: signal sequence #status predicted <SIG>

F,22-146/Product: phospholipase A2 #status predicted <MAT>

F,68,113/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.6%; Pred. No. 3.5e-25;
Matches 62; Conservative 14; Mismatches 47.
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                                                                Accession: S10333
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Search completed: July 3, 2004, 05:18:13 Job time : 11.6755 secs H

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3, 2004, 05:12:38 ; Search time 8.81887 Seconds (without alignments) 726.242 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  OM protein - protein search, using sw model
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722 1 NLVQFGVMIEKMTGKSALQY......YNRKYAHYPNKLCTGPTPPC 123 US-10-088-092A-30\_COPY\_20\_142 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	рошоц	mus n			P21789 cerastes ce						trin	P31482 mus musculu	trin									trimeresu			P20249 agkistrodon								Q90w39 trimeresuru
SUMMAKIES	ΩI		PA2E MOUSE	PA21_ERIMA		PA2 CERCE	PA2N VIPAA	PA2 DABRR	PA21 AGKPI	PA2A_RAT	PA2Q_TRIFL	PA2Y TRIFL	PA2A MOUSE	PA2A_TRIFL	PA2 BITCA	PA2X TRIFL	PA24_AGKHP	PA28_VIPPA	PA29_AGKHP	PA2B_TRIFL	PA2W_TRIFL	PA21_BOTJR	PA26_TRIGA	PA2B VIPAA	PA28 DABRR	PA22_AGKHA	PA2_VIPBB	PA2A VIPAA	PA2C_VIPAA	PA22_TRIGA	PA21 AGKHA	PA2 TRIJE		PA2A_TRIMU
	DB	-	-	-	٦	Н	н	н	-				Н	٦	٦	-	٦	н	Н	ч	Н	-1	н	Н	Н	Н	н					-	Н	7
	Length	142	142	121	144	120	137	121	123	146	138	138	146	122	121	122	138	137	122	122	138	138	138	138	121	122	122	138	138	122	122	138	138	138
. do (	Query	100		51.	49	49.	49.	49.	48.	48.	47.	47.	47.	47.	47.	47.0	47.	47.	46.	46.	46.	46.	46.	46.	46.	46.	46.	45.	45.	45.	45.	45.	45,2	4
	Score	722	662	372	360.5	28	358	355	350	347	44	344.5	341	340.5	340	339.5	339.5	339	338.5	338.5	337.5	335.5	334.5	333.5	332.5	332.5	332.5	330.5	330.5	329.5	328.5	327.5	326.5	326.5
j,	Result No.	н	6	m	4	S	φ	7	ω	סי	10	11	12	13	14	15	16	17	18	19	20	21	. 25	23	24	52	56	27	28	59	30	31	32	33

P24294 eristocophi	042192 agkistrodon	Q92147 trimeresuru	P81480 trimeresuru	P59171 echis ocell	042190 agkistrodon	P47711 cavia porce	P14421 agkistrodon	Q91506 trimeresuru		P18998 crotalus sc	P20474 bothrops as
PA22_ERIMA	PA28 AGKHP	PA2P_TRIFL	PA23 TRIGA	PA25_ECHOC	PA26 AGKHP	PA2M_CAVPO	PA23 AGKHP	PA21_TRIMU	PA21_TRIGA	PA2A_CROSS	PA21_BOTAS
Н	Н	Н	Н	Н	н	<del>, -1</del>	m	н	н	Н	Н
121	122	138	122	138	124	145	122	122	138	138	122
45.1	45.1	45.1	44.9	44.9	44.9	44.9	44.5	44.4	44.3	44.3	44.1
325.5	325.5	325.5	324.5	324.5	324	324	321.5	320.5	319.5	319.5	318.5
34	35	36	37	38	39	40	41	42	43	44	4 5

### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Group IIE secretory phospholipase A2 precursor (RC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GIE) (GIE SPLA2) (sPLA(2)-IIE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.
GO; GO:000644; P:phospholipase A2 activity; TAS.
R GO; GO:000644; P:phospholipaseA2.
R GO; GO:0006644; P:phospholipaseA2.
InterPro; IPR00121; PhospholipaseA2.
R Pfam; PR00089; PHPHLIPASEA2.
R PRMMTS; PR00389; PHPHLIPASEA2.
R PRMMTS; PR00389; PHPHLIPASEA2.
R PRMAT; SM00085; PA2.
R PROSITE; PS00119; PA2. ASP; FALSE_NEG.
R PROSITE; PS00119; PA2. ASP; FALSE_NEG.
R PROSITE; PS00119; PA2. ASP; TALSE_NEG.
R CROWN TALL TALSE ASP; TALSE_NEG.
R CROWN TALL TALSE ASP; TALSE_NEG.
R CROWN TALL TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE ASP; TALSE A
                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 placenta.
-!- SIMILARITY: Belongs to the phospholipase A2 family.
                                                           142 AA
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF189279; AAF36541.1; -.
                                                           STANDARD;
                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P14555; 1POD.
                                                           HUMAN
RESULT 1
PA2E_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KLEKYLPSITRDNIFCAGRTACQRHTCECDKRAALCFRHNINTYNRKYAHYDNKLCTGPT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLEKYLFSVSERGIFCAGRITCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 120
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01-MRR-1992 (Rel. 21, Last sequence update)
10-MR-1903 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme PLA-1 (EC 3.1.1.4) (Phosphatidylcholine
2-acylhydxolase).
Eristocophis macmahoni (Leaf-nosed viper)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Eristocophis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        GROUP IIE SECRETORY PHOSPHOLIPASE A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.7%; Score 662; DB 1; Length 142; 88.6%; Pred. No. 1.6e-64; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
   levels in various other tissues.
-:- SIMILARITY: Belongs to the phospholipase A2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8B0E3CC710A1F946 CRC64;
                                                                                                                                                                                                                                                                                                                                            SMARY; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00118; PA2_HIS; 1.
Inpid degradation; Signal; Calcium. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AA
                                                                                                                                                                                                                                                    MGD; MGI:1349660; Pla2g2e.
InterPro; IPR00121; PhospholipaseA2.
Pfam; PR0068; phoslip; 1.
PRIMY: PR00189; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                  EMBL; AF166098; AAF2499.1; -. EMBL; AF112984; AAF22290.1; -.
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142 AA; 15942 MW;
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AC P2423;
DT 01-MAR-1992
DT 01-MAR-1992
DT 00CT-2003
DE 2-acylhydrollos
DE 2-acylhydrollos
CS Eristocophis
OC Eustaryota; M
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DISULFID
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STRAIN=BALB/C;
MPDLINE=2014878; PubMed=10681567;
Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
Fujii N., Kawamoto K., Hanasaki K.;
Fujii N., Kawamoto K., Hanasaki K.;
"Structures, enzymatic properties, and expression of novel human and
mouse secretory phospholipaes are secretory phospholipaes.";
J. Blod. Chem. 275:5789-5793 (2000).
-:- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
                                                                                                                                                                                                                                                                                                                                                                                                                             20 NLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
                                                                                                                                                                                                                                                                                                                                                                                                      1 NLVQFGVMIEKMTGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE)
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acyl groups in 3-sn-phosphoglycerides.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acyldlycerophosphocholine + a fatty acid anion.
-!- CORACTOR: Binds 1 calcium ion per subunit.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
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; Pred. No. 5.4e-71;
0; Mismatches 0; Indels
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J. Biol. Chem. 274:31195-31202(1999)
                                                                                                                                                                                                                                                                                 66
15989 MW;
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Best Local Similarity '100.0'
Matches 123; Conservative
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PLA2G2A OR PLA2B OR RASF-A OR PLA2L
              Homo sapiens (Human)
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                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human spleen.
 60 PKLEKYLFSVSERGIFÇAGRITÇQRLTÇEÇDKRAALÇFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 PKLSTYSYSFQNGDIVCGDDNACLRAVCECDRVAAICFGENINTYDRKYKDYPSSQCT-E 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLYQPGKMIFKMTGKSALLSYSDYGCYCGWGGKGKPLDATDRCCPVHDCCYGRVN--GCN 58
                                                                                   macmahoni) venom.";

Bur. J. Biochem. 201:675-679(1991).

-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.

-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
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P1455; QUICD2;
01-JAN-1990 (Rel. 13, Created)
01-AR-2090 (Rel. 14, Last sequence update)
15-MAR-2094 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-Mar-2019 (Rel. 43, Last annotation update)
16-Mar-2019 (Rel. 43, Last annotation update)
16-Mar-2019 (Rel. 43, Last annotation update)
16-Mar-2019 (Rel. 43, Last annotation update)
16-Mar-2019 (Rel. 43, Last annotation update)
16-Mar-2019 (Rel. 43, Last annotation update)
(GIC SPLA2) (Non-pancreatic secretory phospholipase A2)
                               MEDLINE=92037623; PubMed=1935962; Siddig1 A.R., Zaidi Z.H., Joernvall H., "Purlification and characterization of two highly different group II phospholipase A2 isozymes from a single viperid (Eristocophis macmahoni) venom.";
                                                                                                                                          acylglycerophosphocholine + a fatty acid anion.
-!-CAFATOR: Binds 1 calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 372; DB 1; Length 121;
Pred. No. 2.8e-33;
8; Mismatches 42; Indels
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
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PROSITE; PS00118; PA2 HIS; 1.
Hydrolase; Lipid degrādation; Calcium; Multigene family.
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InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
PRODOW; PD0003031; PhospholipaseA2; 1.
SWART; SM00085; PA2c; 1.
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Best Local Similarity 56.5%;
Matches 70; Conservative
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PIR; S17860; S17860.
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NCBI_TaxID=8702;
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MEDLINE=2238827; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlanent R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Battow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Jordan T.B., Forland M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Forland M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Forland M.F., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Nilland B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Chenchall S., Willed M. Marra M.A.,
Chenchall S., Willed M. M., Warra M.A.,
Chenchall S., Willed S., Willed M. M., Warra M. M., Warra M. M., Willed M. M., Warra M
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MEDLINE-8931461; PubMed=2775276;
Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
"The primary structure of a membrane-associated phospholipase A2 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99197814; PubMed=3240982; Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.; Matsuta K., Miyamoto T., Inoue K.; Matsuta K., Miyamoto T., Inoue K.; Matsuta K., Miyamoto T., Inoue K.; Matsuta M. Matsuta M. Matsuta M. Matsuta M. Matsuta M. Misamoto M. Matsuta M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. Misamoto M. 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MEDLINE-89174633; Pubmed=2925633;
Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow B.P.,
Tizard R., Pepinsky R.B.;
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Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
"Structure and properties of a secretable phospholipase A2 from human
                                                                                                                                                                                                                                          EDUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

TISSUE-Rheumatoid arthritic synovial fluid;

WEDLINE-89174566; PubMed=2925608;

Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,

Kloss J., Johnson L.K.;

Kloss J., Johnson L.K.;

Rloning and recombinant expression of phospholipase A2 present in rheumatoid arthritic synovial fluid.";

J. Biol. Chem. 264:5335-5338(1989).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structure and properties of a human non-pancreatic phospholipase
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Adv. Exp. Med. Biol. 275:35-53(1990)
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TISSUE-Synovial fluid,
MEDLINE-89076274; PubMed=3202859;
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TISSUE=Synovial fluid;
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69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98207049; PubMed=9538252;

MEDLINE=98207049; PubMed=9538252;

Aitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;

Aitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;

MICTYSEAL STRUCTURE of human secretory phospholipase A2-IIA complex

With the potent indolizine inhibitor 120-1032.";

J. Blochem. 123:19-622 (1998).

J. Blochem. 123:19-622 (1998).

J. Blochem. 123:19-620 (1998).

J. Blochem. 123:19-620 (1998).

J. Blochem. 123:19-620 (1998).

J. C. Province in J. Phospholipae in the regulation of the phospholipid metabolism in biomembranes including eicosanoid biosynthesis: Catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-an-phospholycerides.

J. C. CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

J. COFACTOR: Binds I calcium ion per subunit.

J. SUBCELLULAR LOCATION: Membrane-associated.

J. MISCELLULAR LOCATION: Membrane-associated.

J. MISCELLULAR LOCATION: Membrane-bound and secreted forms are identical and are encoded by a single gene.

J. SIMILARITY: Belongs to the phospholipase A2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X.-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=95393225; PubMed=7664108;
Schevitz R.w., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihellch B.D.,
Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
"Structure-based design of the first potent and selective inhibitor
of human non-pancreatic secretory phospholipase A2.";
Nat. Struct. Biol. 2:458-465(1995).
                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=91287826; PubMed=2062381;
Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
Merlich G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
Warrick M.W., Jones N.D.;
"Structure of recombinant human rheumatoid arthritic synovial fluid
phospholipase A2 at 2.2-A resolution.";
                                                                                                                                    MEDLINE=94002200; PubMed=8399335; Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.; Purification and characterization of a phospholipase A2 from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sigler P.B.; "Structures of free and inhibited human secretory phospholipase A2
    Lai C.Y., Wada K.; "Phospholipase A2 from human synovial fluid: purification and structural homology to the placental enzyme."; Biochem. Biophys. Res. Commun. 157:488-493(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92054586; PubMed=1948070;
Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
                                                                                                                                                                                                                 Biochim. Biophys. Acta 1170:125-130(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M22430; AAA36550.1; -.
EMBL; M22431; AAA36549.1; -.
EMBL; BC005319; AAH05919.1; -.
PIR; A32862; PSHVYF.
PDB; LAYP; 31-JUL-95.
PDB; 1BBC; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from inflammatory exudate.";
Science 254:1007-1010(1991).
                                                                                                                      TISSUE=Ileal mucosa;
                                                                                                   SEQUENCE OF 21-75
                                                                                                                                                                                                 ileal mucosa.";
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1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
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PA2 CERCE
1D PA2_CERCE STANDARD; PRT; 120 AA.
AC P21789;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last annotation update)
DE phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS Cerastes cerastes (Horned desert viper).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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BY SIMILARITY.
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CALCIUM (VIA CARBONYL OXYGEN).
CALCIUM (VIA CARBONYL OXYGEN).
CALCIUM.
                                                                                               Probon, PD000303, PhospholipaseA2; 1.
SMART; SM00085, PA2c; 1.
PROSITE; P800119; PA2_HIS; 1.
PROSITE; P800119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
GO, GO:0004623; F:phospholipase A2 activity; TAS.
InterPro; IPR00121; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
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SEQUENCE FROM N.A.
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NLYQEGKMIFKMTGKSPIFSYGDYGCYCGWGGKGTPVDATDRCCEVHDCCYGRVN--SCN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 PKLEKYLFSVSERGIFCAGRITCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCT 117
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SEQUENCE OF 1-31.
STRAIN=TURISIA: TISSUE=Venom;
STRAIN=TURISIA: TISSUE=Venom;
MEDLINE=90388487; PubMed=2402760;
Djebari F.L., Martin-Eauclaire M.-F.;
"Purification and characterization of a phospholipase A2 from Cerastes cerastes (horn viper) snake venom.";
Toxicon 28:637-646(1990).
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + afatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATIVIN: Secreted.
                                                                                                MEDLINE=91130587; PubMed=1993470;
Siddigi A.R., Shafqat J., Zaidi Z.H., Joernvall H.;
"Characterization of phospholipase A2 from the venom of Horned viper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANEOUS: Strains variations are extensive for this enzyme. -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Cerastes.
NCBI_TaxID=8697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.7%; Score 358.5; DB 1; Length 120;
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PIF -> ALL (IN STRAIN TUNISIA).

BESSIFA7001C62C3 CRC64;
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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live 10; Mismatches 41; Indels
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PIR; A35950; A35950.

PIR; S13019; S13019.

HSSP; P81458; 1VIP.

InterPro; IPRO01211; PhospholipaseA2.

PRODM; PR00189; PHPHILIPASEA2.

ProDom; P0000303; PhospholipaseA2; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS001118; PA2_HIS; 1.

PROSITE; PS001118; PA2_HIS; 1.

Hydrolase; Lipid degradation; Calcium.

ACT_SITE #7 47 47 BY SIMILARI

DISULFID 26 115 BY SIMILARI
DISULFID 28 SIMILARI
DISULFID 43 95 BY SIMILARI
DISULFID 50 B8 BY SIMILARI
DISULFID 50 B8 BY SIMILARI
                                                                                      STRAIN=Baluchistan; TISSUE=Venom;
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                                                                                                                                               (Cerastes cerastes).";
FEBS Lett. 278:14-16(1991).
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120 AA;
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                                                                                                                                                                                                                                                                                                                                                                      "Amino acid and cDNA sequences of a neutral phospholipase A2 from the long-nosed viper (Vipera ammodytes ammodytes) venom."; Eur. J. Biochem. 204:1057-1062(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the caryl groups in 3-sn-phosphoglycerides.

-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.

-!- CORACTOR: Binds I calcium ion per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kordis D., Gubensek F.;
"Molecular evolution of phospholipase A2 multigene family in Vipera
                                                                                                                                                                 Vipera ammodytes ammodytes (Western sand viper).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Viperinae; Vipera.
PAZN VIPAA

DA PAZN VIPAA

AC F34180; Q5167;

AC F34180; Q5167;

DT 16-0CT-2001 (Rel. 40, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

To mendytes (Western sand viper).
                                                                                                                                                                                                                                                                                                                           Krizaj I., Liang N.-S., Pungercar J., Strukelj B., Ritonja A., Gubensek F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pungercar J.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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InterPro; 1PR001211; PhospholipaseA2.
InterPro; 1PR001211; PhospholipaseA2.
Pfam; PF00068; Phoslip; Propom; P000039; PHPLIPASEA2.
ProDom; P0000303; PhospholipaseA2; 1.
PROSTIE; PS00119; PA2c; 1.
PROSTIE; PS00119; PA2c, ASP; 1.
PROSTIE; PS00119; PA2_HIS; 1.
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MEDLINE=92201190; PubMed=1551386;
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EMBL; X84018; CAA58840.1; -.
PIR; S22388; S22388.
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Best Local Similarity 53.28
Matches 66; Conservative
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A Carredano B., Westerlund B., Persson B., Saarinen M., Ramaswamy S.,
Carredano B., Westerlund B., Persson B., Saarinen M., Ramaswamy S.,
Eaker D., Eklund H., Persson B., Saarinen M., Ramaswamy S.,
Three three-dimensional structures of two toxins from snake venom
throw light on the anticoagulant and neurotoxic sites of
throw light on the anticoagulant and neurotoxic sites of
Toxicon 36:75-92(1998).
I Toxicon 36:75-92(1998).
I Toxicon 36:75-92(1998).
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I Toxicon 36:75-92(1998).
I Toxicon 10:75-92(1998).
I Toxicon 10:7
                                                                                                                                                                                                                                                                      60 PKLEXYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                    75 PKLSIYSYSFENGDIVCGGDDPCLRAVCECDRVAAICFGENLNIYDKKKNYPSSHCT-E 133
                                                                                                                                                                                                                               17 NLYQFGNMIFKMTKKSALLSYSNYGCYCGWGGKGKPQDATDRCCFVHDCCYGRVN--GCD 74
                                                                                                                                                                                                               59
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Daboia.
                                                                                                                                                                                                               1 NLVQFGVMIEKWIGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                     4.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phospholipase A2 RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-
BY SIMILARITY.

CALCIUM (IVA CARBONYL OXYGEN)

(BY SIMILARITY).

CALCIUM (VIA CARBONYL OXYGEN)

(BY SIMILARITY).

CALCIUM (VIA CARBONYL OXYGEN)

(BY SIMILARITY).

CALCIUM (IN SIMILARITY).

CALCIUM (IN SIMILARITY).

CALCIUM (IN SIMILARITY).

CALCIUM (IN SIMILARITY).
                                                                                                                                                      49.6%; Score 358; DB 1; Length 137; 54.8%; Pred. No. 1e-31; Live 11; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMARY; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HIS; 1.
Agrolase; Lipid degradation; Calcium; 3D-structure.
ACT_SITE 89 89
                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA.
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PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1VIP; 16-JUN-97.
InterPro; IPR001211; PhospholipaseA2
                                                                                                                            15309 MW;
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Conservative 1
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43
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137 AA;
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les 68; Conserv
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60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
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MEDINIDE-9327049; PubMed=8489705;
MEININE-9327049; PubMed=8489705;

"An examination of structural interactions presumed to be of importance in the stabilization of phospholipase A2 dimers based upon comparative protein sequence analysis of a monomeric and dimeric enzyme from the venom of Agkistrodon p. piscivorus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLFQFAEMIVGMTGKNPLSSYSDYGCYGWGGKGKPQDATDRCCFVHDCCYEKVK--SCK
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PA21_AGKPI STANDARD; PRT; 123 AA.

01-0CT-1996 (Rel. 34, Created)

15-UUL-1998 (Rel. 36, Last sequence update)

10-CCT-2003 (Rel. 42, Last annotation update)

Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)

Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)

(APP-D-49).

Agkistrodon piscivorus piscivorus (Eastern cottonmouth).

Agkistrodon piscivorus piscivorus, (Eastern Cottonmouth).

Lepidosauria, Squamata, Craniata; Vertebrata; Buteleostomi;

Lepidosauria, Squamata, Scleroglossa, Serpentes; Colubroidea;

Viperidae, Crotalinae; Agkistrodon.
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CALCIUM (VIA CARBONYL OXYGEN)
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(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA SIMILARITY).
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53.2%; Pred. No. 1.9e-31;
tive 13; Mismatches 41
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                                                                             TISSUE=Venom;
MEDLINE=85054816; PubMed=6438084;
Marganore J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,
Maraganore J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,
Heinrikson R.Li.;
"A new class of phospholipases A2 with lysine in place of aspartate
49. Functional consequences for calcium and substrate binding.";
J. Biol. Chem. 259:13839-13843(1984).
                                                                                                                                                                                                                                                  subfamily.
PIR: B33872, B53872.
PDB: 1VAP: 07-JUL1; PhospholipaseA2.
EASH PROUDLI; PhospholipaseA2.
PRINTS; PRO0389; PHPHLIPASEA2.
PRINTS; PRO0389; PhospholipaseA2; 1.
PROFORS; PAC: 1.
PROSTER; SMO00303; PhospholipaseA2; 1.
PROSTER; PSO0119; PA2_ASP; 1.
PROSTER; PSO0118; PA2_HSP; 1.
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CALCIUM (VIA CARBONYL OXYGEN)
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CALCIUM (VIA CARBONYL O
CALCIUM.
N(6)-palmitoyl lysine.
N(6)-palmitoyl lysine.
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                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
Protein Chem. 12:187-193(1993).
            SEQUENCE OF 1-23, AND ACYLATION.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDIINE=89350908; PubMed=2764915;
Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.,
Yoshida N., Teraoka H., Tojo H., Okamoto M.;
"COBA cloning and sequence determination of rat membrane-associated phospholipase A2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN 1990 (Rel. 13, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phospholipase A2, membrane associated precursor (BC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                           4;
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MEDLINE=90110043; PubMed=2606907;
Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;
"Structure of cDNA coding for rat platelet phospholipase A2.";
J. Biochem. 106:545-547(1989).
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MEDLINE=90381322; PubMed=2400792;
Kusunoki C., Satch S., Kobayashi M., Niwa M.;
"Structure of genomic DNA for rat placelet phospholipase A2.";
Biochim. Biophys. Acta 1087:95-97(1990).
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"Structure of gene coding for rat group II phospholipase A2.";
Biochem. Biophys. Res. Commun. 168:1059-1065(1990).
                                                                                                                                                                                                                                                                                                 Length 123;
                                                                                                                                                                                                                                                                                                                                                        42; Indels
                                                                                                                                                                                                                                              13989 MW; C39986552D990D72 CRC64;
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                                                                                                                                                                                                                                                                                              48.5%; Score 350; DB 1; 52.0%; Pred. No. 6.8e-31; iive 14; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AA
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MEDLINE=90267443; PubMed=2346480;
                                                                                                                                                                                                                                                                                                                                                        65; Conservative
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113 J
                                                                                                                                                                                                                                                                                                                        Similarity
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RX MEDLINES 89255484; PubMed=2722857;

RA Aarsman A.J. de Jong J.G.N. Annoldussen E., Neys F.W.,

RA van Wassenaar P.D., van den Bosch H.;

RT "menunodfinity purification, partial sequence, and subcellular

RT localization of rat liver phospholipase A2.";

RL J. Biol. Chem. 264:10008-10014 [1989].

CC "I FUNCTION THOUGH to participate in the regulation of the phospholipid metabolism in biomembranes including eicosanoid biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-carl groups in 3 sn-phospholipine + H(2)0 = 1-carl groups in 3 sn-phospholine + a fatty acid anion.

CC "I CARALYTIC ACTIVITY: PhosphatidyLcholine + CC acyl groups in 3 sn-phospholipine + a fatty acid anion.

CC "I CARALYTIC ACTIVITY: PhosphatidyLcholine + CC acyl groups in Calcium ion per subunit (By similarity).

CC "I CARCELLANBOUS: Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene.

CC "I SIMILARITY: Belongs to the phospholipase A2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.; "Amino acid composition and NH2-terminal amino acid sequence of rat platelet secretory phospholipase A2."; J. Blochem. 101:1311-1314(1987).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                        Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;
Purification and Characterization of a membrane-associated
phospholipase A2 from rat spleen. Its comparison with a cytosolic
phospholipase A2 S-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, D00523; BAA00410.1; -.

EMBL, M37127; AAA41223.1; -.

EMBL, M31344, A33390.1; -.

PRE, A33394, A33394.

PRESP, P14555; 1D001211; PhospholipaseA2.

Incerpro, IPR001211; PhospholipaseA2.

ProDom; PR00083; PHPHLIPASEA2.

ProDom; PR00189; PA2C, 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

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PROSITE; PS00119; PA2_ASP; 1.

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PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00119; PA2_ASP; 1.
SEQUENCE OF 22-146.
STRAIN=Wistar; TISSUB=Platelet;
MEDLINE=89174508; PubMed=3235451;
Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
"The primary structure of rat platelet phospholipase A2.";
J. Biochem. 104:767-772 (1988).
                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 263:5732-5738(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Platelet;
MEDLINE=88007474; PubMed=3654593;
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MEDLINE=88186890; PubMed=3356705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 PXLEKYLFSVSERGIFCA-GRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phospholipase A(2) isozymes.";

J. Mol. Evol. 56:286-293(2003).

J. Mol. Evol. 56:286-293(2003).

J. CALTALTIC SALE ACTIVITY: Phosphacidy. The calcium dependent hydrolysis of to capaly groups in 3-sn-phosphoglycerides.

J. CARALTIC ACTIVITY: Phosphacidy. H(2)0 = 1-acyl groups in 9-sn-phospholine + H(2)0 = 1-cacyl groupsphospholine + a fatty acid anion.

J. COFACTOR: Binds 1 calcium ion per subunit (By similarity).

J. SURGELBULAR LOCATION: Secreted (Probable).

J. TISSUE SPECIFICITY: Expressed by the venom gland.

J. SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I., Nakashima K.-I., Oda-Ueda N., Pukumaki Y., Hattori S., Ohno M.; "Interisland evolution of Trimeresurus flavoviridis venom
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
CALCIUM (VIA CARBONYL OXYGEN)
CALCIUM (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                           48.1%; Score 347; DB 1; Length 146; ilarity 51.2%; Pred. No. 1.7e-30; Conservative 14; Mismatches 45; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
10-COT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme cPLA+B (A) precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase).
                                                                                                                                                                                                          (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
P -> L (POLYMORPHISM).
S -> D (IN REF. 8).
W -> E (IN REF. 5).
D -> E (IN REF. 5).
R -> S (IN REF. 5).
L -> V (IN REF. 5).
A -> S (IN REF. 5).
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MEDLINE-22499762; PubMed-12612832;
                                                                                                                                                                                                                                                                                                                                                                                                       60DDC9E79BF109F7 CRC64;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
(CALCIUM (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-Inmeresurus flavoviridis (Habu).
11-Inmeresurus flavoviridis (Habu).
12-Inmeresurus, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
13-Inmeresuria, Squamata; Scleroglossa; Serpentes; Colubroidea;
13-Inmeresurus.
13-Inmeresurus.
13-Inmeresurus.
13-Inmeresurus.
13-Inmeresurus.
                                                                                          InterPro; IPR001211; PhospholipaseA2.
PRINTS; PR00088; phoslip; 1.
PRINTS; PR00089; PhospholipaseA2; 1.
SWART; SW00085; PA2c; 1.
SWART; SW00085; PA2c; 1.
PROSITE; PS00118; PA2 ASP; 1.
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    47.7%; Score 344.5; DB 1; Length 138; 50.0%; Pred. No. 3e-30; tive 15; Mismatches 44; Indels 3
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CALCIUM (VIA CARBONYL OXYGEN)
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CALCIUM (BY SIMILARITY).
CEDES40581DD2F10 CRC64;
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                                                                                    EMBL; AB087496; BAC02719.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 50.0 62; Conservative
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138 AA;
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-1. FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
-1. CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphochline + a fatty acid anion.
-1. COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-1. SUBCELLULAR LOCATION: Secreted (By similarity).
-1. TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
-1. SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000103; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2 ASP; 1.
PROSITE; PS00118; PA2—HIS; 1.
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
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01-JUL-1993 (Rel. 26, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
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PHOSPHILPASE A2 ISOZYME PL-Y.

BY SIMILARITY.

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CALCIUM (BY SIMILARITY)
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Pfan; PR00068; phoslib; 1.
PRINTS: PR00389; PHPHI.PASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
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PAZA_MOUSE
ID _PAZA_M
AC P31482
DT 10-UUL
DT 15-MAR
DE Phospho
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47.2%;
52.8%;
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113
139
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19
86
146 AA;
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Best Local Similarity
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MEDINE=2288257; PubMed=12477932;
MEDINE=2288257; PubMed=12477932;
MEDINE=2288257; PubMed=12477932;
MEDINE=2288257; PubMed=12477932;
MALSTER R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heng L.,
Brapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,
Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Braha S.S., Morden P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boufface S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Gaber E. Human D.M., Marra M.A.,
"Gaber E. Human D.M., Marra M.A.,
"Green E.D., Smirk M. Marra M.A.,
"Green E.D., Smirk M. Marra M.A.,
"Green E.D., Smirk M. Marra M.A.,
"Green E.D., Smirk M. Marra M.A.,
"Green E.D., Smirk M. M.,
"Green E
                                                                                                                                                                                                    SEQUENCE FROM N.A., AND POLYMORPHISM.
STRAIN=BALB/C, and CD-1; TISSUB=Intestine;
MEDLINE=95403435; PubMed=7673223;
Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
Ywan M., Tang C., Rancourt D.E., Cromlish W.;
The Anatural disruption of the secretory group II phospholipase A2 gene
in inbred mouse strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/C; TISSUE-Small intestine;
MEDINTE=9402955; PubMed=8267767;
MULNTE=9402955; PubMed=8267767;
MULNTE=9402955; PubMed=8267767;
"Enhancing factor, a Paneth cell specific protein from mouse small intestines: predicted amino acid sequence from RT-PCR amplified cDNA and its expression.";
Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
                                                                                                                                                                                                                                                                                                                                                                                                           MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D., Buchberg A.M.,
Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                        "The secretory phospholipase A2 gene is a candidate for the Moml
locus, a major modifier of ApcMin-induced intestinal neoplasia.";
Cell 81:957-966(1995).
                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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TISSUE-Small intestine;
MEDLINE-3146.72; PubMed-8425615;
Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;
                                                                                                                                              STRAIN=BALB/c_i
Mulherkar R.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
Biochem. Biophys. Res. Commun. 197:351-352(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                              Biol. Chem. 270:22378-22385(1995).
                 sPLA2) (Enhancing factor) (EF)
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                                                Mus musculus (Mouse).
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14054 MW;
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122 AA;
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P00622;
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Best Local S:
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-!- FUNCTION: PAZ catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Displays edema-inducing activities. PLA-A is three times less active than PLA-B in edema-
                        60 PKLEKYLFSVSERGIFC-AGRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTG
             1 NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
Gaps
                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme PLA-A, basic (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase).
Trimeresurus, flavoviridis (Habu).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                               Hattori S., Ohno M.;
"Characterization, amino acid sequence and evolution of edema-
inducing, basic phospholipase A2 from Trimeresurus flavoviridis
venom.";
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                                                                                                                                                                                                                            -1-INGUALIZATIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
-1-CORACTOR: Binds I calcium ion per subunit (By similarity).
-1-SUBCELLULAR LOCATION: Secreted.
-1-TISSUE SPECIFICITY: Expressed by the venom gland.
-1-TISSUE SPECIFICITY: Expressed by the venom gland.
-1-SIMILARITY: Belongs to the phospholipase A2 family. Group
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                                                                                                                                122 AA.
Mismatches
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66; Conservative
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PA2A TRIFL
ID PA2A TRIFL
AC P59264;
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                                                                                                                                                                                                                                                                                    TISSUE-Venom, MEDLINES-830452262; PubMed=7135414; MEDLINES-830452262; PubMed=7135414; Viljoen C.C., Botes D.P., Kruger H.; Viljoen C.C., and amino acid sequence of caudoxin, a presynaptic acting toxic phospholipase A2 from the venom of the horned puff adder (Bitis
                                                                                                                                                                                                                                                           60 PKLEKYLFSVSERGIFCAGRTTCQRLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP
                                                                                                                                                               1 NLVQFGVMIEKMTGKSAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
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Bitis caudalis (Horned adder) (Horned viper).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Bitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 02, Last ennotation update)
Phospholipase A2 (EC 3.1.1.4) (Caudoxin) (Phosphatidylcholine 2-
                                                                                                                3,
                                                                     DB .1; Length 122;
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R HSSP, P81459.

R HSSP, P81459.

R InterPro. J PR001211, PhospholipaseA2.

R Fam; PF00068; phoslip; 1.

R PRINTS; PR001389; PHPHLIPASEA2.

R PRODOM; P800199; PA2c; 1.

R PROSITE; P80019; PA2 ASP; 1.

R PROSITE; P80019; PA2 ASP; 1.

R PROSITE; P80019; PA2 ASP; 1.

R PROSITE; P80018; PA2 ASP; 1.

R Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin; Presynaptic neurotoxin.

R ACT_SITE 46 46 BY SIMILARITY.

R ACT_SITE 88 BY SIMILARITY.

R DISULFID 25 114 BY SIMILARITY.
                                                                                                                  43; Indels
CALCIUM (BY SIMILARITY).
250EB22761E662E9 CRC64;
                                                                47.2%; Score 340.5; DB 1
49.2%; Pred. No. 7.1e-30;
tive 17; Mismatches 43
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MBDLINE=G7179112; PubMed=3564060;
Kini R.M., Kawabata S.-I., Iwanaga S.;
Kini R.M., Kawabata S.-I., Iwanaga S.;
Kini R.M., Kawabata S.-I., Iwanaga S.;
Comparison of amino terminal region of three isoenzymes of phospholipases A2 (TFV PL-Ia, TFV PL-Ib, TFV PL-X) from Trimeresurus flavoviridis (habu snake) venom and the complete amino acid sequence of the basic phospholipase, TFV PL-X.";
CAX.CON 24:1117-1129(1966).
-i. FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLVQFGVMIEKMIGKSALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCEP
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01-JAN-1988 (Rel. 06, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 isozyme PL-X (BC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trimerseurus flavoviridis (Habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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--- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acyldlycerophosphocholine + a fatty acid anion.
--- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- INSUE SPECIFICITY: Expressed by the venom gland.
--- SIMIGARITY: Belongs to the phospholipase A2 family. Group II
BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
(CALCIUM (VIA CARBONYL OXYGEN)
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PIR, ASSOO, PSTVXF.

HSSP, P51972, 1VAP.

InterPro, 1PR001211; PhospholipaseA2.

InterPro, 1PR001211; PhospholipaseA2.

Pfam, PF00068; phoslip; 1.

PRINTS, PR00389; PHPLILPASEA2.

ProDom; P000033; PhospholipaseA2, 1.

PROSITE; PS00119; PA2_ASP; PALSE_NEG.

PROSITE; PS00118; PA2_HIS; 1.

Hydrolase; Lipid degradation; Calcium; Multigene family.

Hydrolase; Lipid degradation; Calcium; Multigene family.

ACT_SITE 47 47 BY SIMILARITY.

DISŪLFID 26 115 BY SIMILARITY.
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47.1%; Score 340; DB 1;
Best Local Similarity 47.2%; Pred. No. 8e-30;
Matches 58; Conservative 15; Mismatches 4
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89
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                                                                                                                                                                  Query Match

47.0%; Score 339.5; DB 1; Length 122;
Best Local Similarity 49.2%; Pred. No. 9.2e-30;
Matches 61; Conservative 16; Mismatches 44; Indels 3
BY SIMILARITY.
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BY SIMILARITY.
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (SY SIMILARITY).
CALCIUM (SY SIMILARITY).
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COMPUTER READBLE FORM:
MODIVIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,360
FILING DATE: 03-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tseng, Albert P. S.
APPLICANT: Tseng, Albert P. S.
APPLICANT: Inglis, Adam
APPLICANT: Inglis, Adam
APPLICANT: Inglis, Adam
ADDESSER OF SEQUENCES:
ADDESSES: Rochwell, Figg Ernst & Kurz
STRET: Suite 701-E, 555 Thirteenth St., N.W
STATE: D. C.
COUNTRY: U.S.A.
                                PCT-US94-07926-14
US-08-888-497-30
US-09-36-230-30
US-08-966-317-1
US-09-489-770-1
US-09-362-230-43
US-09-362-230-43
US-09-362-230-43
US-09-362-230-43
US-09-888-497-22
US-09-888-497-22
US-09-888-497-22
US-09-888-497-22
US-08-888-497-22
US-09-09-0602-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULBASIFICATION DATA:
PURBLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-UUL-1992
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: AU PK 7058
FILING DATE: 04-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: ETISE, BATBARG G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-104A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08170360
Patent No. 5656602
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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STRANDEDNESS:
TOPOLOGY: line
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HYPOTHETICAL: N
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US-08-170-360-4
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722
1 NLVQFGVMIEKWIGKSALQY......xnrkyAHYPNKLCTGPTPPC 123
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Sequence
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/cgn2 6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/2/jaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-888-497-39
US-09-7460-569-2
US-09-7460-569-2
US-08-186-895-110
US-08-186-895-110
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US-08-186-895-110
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US-08-186-110-13
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US-09-186-110-14
US-09-186-110-14
US-09-186-110-14
US-08-186-110-14
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                                                                                                                                                                                                                           389414 segs, 51625971 residues
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                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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JS-09-362-230-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian/Phospholipase A2 Nuglectide
TITLE OF INVENTION: Mammalian/Phospholipase A2 Nuglectide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Tibosome Binding Sites
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                        1 NLVNPHRMIKLTTGKEAALSYGFYGCHCGVGCRGSPKDATDRCCVTHDCCYKRLEKRGCG 60
                                                                                  1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                            1; Gaps
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49.9%; Score 360.5; DB 2; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1
  DB 1; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                          45;
Score 360.5; DB 1
Pred. No. 1.3e-31;
9; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UTL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/08888497
Patent No. 5972677
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 39:
Query Match
Best Local Similarity 55.6%;
Matches 69; Conservative
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59

1 NLVQFGVMIEKNTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE

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GENERAL INFORMATION:

APPLICANT: Tiscpffeld, Jay A.

APPLICANT: Tiscpffeld, Jay A.

APPLICANT: Sethamer, Jeffrey

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide

TITLE OF INVENTION: Bequences and Low Molecular Meight Amino Acid Sequences

TITLE OF INVENTION: Bequences and Nucleotide

TITLE OF INVENTION: Sequences Naving Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &

ADDRESSEE: Russell PA
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                                                                                   61 TKFLSYKPSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
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                                                    60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
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1 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: ISN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
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Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PROOR APPLICATION DATA:
APPLICATION NUMBER: 08/88,497
FILING DATE: WOMBER: US 08/097,354
APILICATION WUMBER: 26-ULL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
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                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/09362230 Patent No. 6352849
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REGISTRATION NUMBER: 32,264
REFRENCE/DOCKET NUMBER: IN21(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: si
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60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TYFLSYKPSNSGSRITCAKODSCRSQLCECDKAAATCFARNKTIYNKKYQYXSNKHCRGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.9%; Score 360.5; DB 5; Length Best Local Similarity 55.6%; Pred. No. 1.3e-31; Matches 69; Conservative 9; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MEALINGOUS
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,895
FILING DATE: 27-JAN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/046,383
FILING DATE: 09-APR-1993
APPLICATION NUMBER: US/08/046,383
FILING DATE: O9-APR-1993
ATORNEY/AGENT INFORMATION:
NAME: KOKulis, Paul N.
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
TELECOMMUNICATION INDERATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hollis, Melvyn
APPLICANT: Needham, Maurice R.C.
APPLICANT: Gooding, Clare
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: Expression Systems
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Cushman, Darby & Cushman
1615 L Street, N.W.
                                                                                     REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08186895
Patent No. 5538885
GENERAL INFORMATION:
                                                                                                                                                              TELEFA: 305-527-2498
TELEFA: 305-64-4996
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
STRANDEDNESS: single
          FILING DATE: 26-JUL-1993
ATTORNEY, AGENT INFORMATION:
NAME: Manso, Peter J.
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US94-07926-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-822-0944
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                                                                                                                                                         Sequence 2, Application US/09740569
Sequence 2, Application US/09740569
Patent No. 6475484
Patent No. 6475484
APPLICANT: Weiss, Jerrold
APPLICANT: Lisadh, Peter
APPLICANT: Lisadh, Peter
APPLICANT: Lisadh, Peter
APPLICANT: Lisadh, Ning-Sheng
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
TITLE OF INVENTION NUMBER: US/09/740,569
CURRENT PILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: US 60/172,467
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
ERNOR APPLICATION OF 25
SEQ ID NO 2
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKKTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLYNPHRLIKLITGKEAALSYGFYGCHCGYGGRGSPKDATDRCCVTHDCCYKRLEKRGCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NLVOFGVMIEKMTGK-SALOYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STALE.
COUNTRY: USA
ZIF: 33301
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US94/07926
PTT.NG DATE: 15-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.9%; Score 360.5; DB 4
54.8%; Pred. No. 1.3e-31;
tive 11; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-740-569-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 68; Conserv
TPPC 123
                                            TPRC 124
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MOLECULE TYPE: protein
                                                                                    Best Local Similarity
Matches 69; Conserv
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       ; MULECULE ...
US-08-888-497-37
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STATE:
                                                                 Query Match
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Sequence 37, Application US/0888497

Patent No. 5972677

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide

TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                               60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
                                                                                                                                                                                                                                                                                                                                                                                                       1 NLVQFGVM1EKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
                                                                                                                                                                                                                                                                                                                  21 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKLEKAGCG
                                                                                                                                                                                                Length 144;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROFILEDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,497
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                Query Match

49.9%; Score 360.5; DB 1
Best Local Similarity 55.6%; Pred. No. 1.5e-31;
Matches 69; Conservative 9; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: us/us/19651,405
PILING DATE: APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter I'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 305-764-4930
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TELEX: 6714627 CUSH
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-186-895-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TPPC 123
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES 44
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Ruseil PA
                                                                                                                                                                                                                                                   81 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 140
                                                                                                                                             21 NLVNFHRMIKLITIGKBAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGGG 80
                                                                                                              1 NLVQFGVMIEXWTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                   60 PKLEKYLFSVSERGIFCAGRITCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP
49.9%; Score 360.5; DB 2; Length 144; llarity 55.6%; Pred. No. 1.5e-31; Conservative 9; Mismatches 45; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/362,230 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 360.5; DB 4;
Pred. No. 1.5e-31;
9; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/09362230 Patent No. 6352849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Manso, Peter J. REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.6%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305-764-4996
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-362-230-37
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TKFVTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAAECFARNKKSYSLKYQFYPNKFCKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLVQFGVMIEKWIGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.2%; Score 348; DB 2; Length 12
51.2%; Pred. No. 2.9e-30;
iive 14; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/651,405
                                                                                                                                                           Sequence 42, Application US/08888497
Patent No. 5972677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: IN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.2<sup>3</sup>
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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120 TPPC 123
                                           141 TPRC 144
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                                                                                                                                       US-08-888-497-42
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                                                                                                                  RESULT 10
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESSORDERS: Adden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
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                                                                                                                                            81 TKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTIYNKKYQYYSNKHCRGS 140
                                                                                                                60 PKLEKYLFSVSERGIFCAGRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
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                    53
                                                                  80
                                                21 NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG
                    NLVQFGVMI EKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.9%; Score 360.5; DB 5; 55.6%; Pred. No. 1.5e-31; cive 9; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-UUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAISO, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application PC/TUS9407926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
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PCT-US94-07926-37
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Best Local
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INFORMATION FOR SEQ ID NO: 42:
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amino acid
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PCT-US94-07926-42
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Best Local Similarity
Matches 64; Conserv
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US-08-888-497-35
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                                                                       APPLICANT: Tisoffield, Jay A.
APPLICANT: Tisoffield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PKLEKYLFSVSERGIFCA-GRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
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PCT-US94-07926-42
; Sequence 42, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Mammalian Phospholipase A2 Nucleotide
                                                                                                                                                                                                                                   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.2%; Score 348; DB 4;
51.2%; Pred. No. 2.9e-30;
tive 14; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J. 264
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-27-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN21044-5
                Sequence 42, Application US/09362230 Patent No. 6352849
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APPLICATION NUMBER: 08/888,497
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Best Local Similarity 51.2%
Marches 64; Conservative
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MOLECULE TYPE: protein
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                                                        GENERAL INFORMATION:
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US-09-362-230-42
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TITLE OF INVENTION: Sequences and two Molecular Weight Main Acid Sequences and Molecules Sequences and Molecules TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites (WINSMERSEE: Russell PA).

WINSMERSEE: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Russell PA).

STREET: 200 Zaat Broward Boulevard (TITLE OF MOLECULE).

STREET: 200 Zaat Broward Boulevard (TITLE OF MOLECULE).

STREET: ADDRESSEE: Russell PA).

COMPUTES: TROP Companies FOWN.

MONTHS: FILL FOWN AND MOLECULES.

COMPUTES: TROP COMPANIES FOWN.

MONTHS: FILL FOWN AND MOLECULES.

ADDRESSEE: Addressee: Addressee: All Companies Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee: Addressee:
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PKLEKYLFSVSERGIFCA-GRITCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 TKFVTYKFSYRGGOISCSTNODSCRKOLCQCDKAAAECFARNKKSYSLKYOFYPNKFCKG 141
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51.2%; Pred. No. 3.5e-30;
tive 14; Mismatches 45; Indels
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ZIP: 33301
COMPUTEN FRAB. ELOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                              US/09/362,230
                                                                                                                                                                                                                                             US 08/097,354
                                         SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
PRIOR APPLICATION:
RECALL APPLICATION DATA:
APPLICATION WINBER: 08/888,497
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US94-07926-35; Sequence 35, Application PC/TUS9407926; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  NAME: Manso, Peter J. 28, 264
REGISTRATION NUMBER: 32, 264
REFERENCE/DOCKET NUMBER: IN21
TELECHONE: 305-27-4498
TELEFEXX: 305-764-4996
  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 51.2
Matches 64; Conservative
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                          OPERATING SYSTEM:
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  COMPUTER:
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APPLICANT: Tischfield, Jay A.

TITLE OF INVENTION: Manalian Phospholipase A2 Nucleotide

TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCES: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSER: Russell PA

STRRET: 200 East Broward Boulevard

CITY: Fort Lauderdale

STRATE: FL

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PKLEKYLFSVSERGIFCA-GRITCORLICECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
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                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFRENCE/POCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/09362230 Patent No. 6352849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Fort Lauderdale
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US-09-362-230-35
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Best Local
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